

NO.	SCORE	MAJOR	LENGTH	NO.	SCORE	MAJOR	LENGTH	NO.	SCORE	MAJOR	LENGTH
1	2323.4	99.9	2325	2	A644009	Sequence	AX644009	3	2320.6	99.8	2340
2	2320.6	99.8	2340	5	AF488550	Homo sapi	AF488550	6	2320.2	99.8	2352
3	2320.2	99.8	2352	2	AX686997	Sequence	AX686997	4	2323.2	91.8	2352
4	2323.2	91.8	2352	5	AX3040968	Homo sapi	AX3040968	7	2122.6	91.3	2376
5	2122.6	91.3	2376	2	AX542069	Sequence	AX542069	8	2122.6	91.3	2376
6	2122.6	91.3	2376	2	AX369231	Sequence	AX369231	9	2110.4	90.8	3496
7	2110.4	90.8	3496	2	AX348090	Sequence	AX348090	10	1876.2	80.7	3226
8	1876.2	80.7	3226	6	BC039156	Mus muscu	BC039156	11	1876.2	80.7	3226
9	1876.2	80.7	3226	6	MWJ225124	Mus muscu	MWJ225124	12	1872.8	73.6	2343
10	1872.8	73.6	2343	6	AF247452	Rattus no	AF247452	13	1712.2	70.5	3154
11	1712.2	70.5	3154	5	BC000066	Homo sapi	BC000066	14	1638.8	70.5	3245
12	1638.8	70.5	3245	5	AX055840	Homo sapi	AX055840	15	1433.4	57.8	2756
13	1433.4	57.8	2756	5	BC028024	Homo sapi	BC028024	16	1431.4	48.7	3737
14	1431.4	48.7	3737	14	AB022927	Oryctolag	AB022927	17	1087.4	46.8	4751
15	1087.4	46.8	4751	2	AX019005	Sequence	AX019005	18	1085.8	46.7	4751
16	1087.4	46.8	4751	2	AX348088	Sequence	AX348088	19	1085.8	46.7	4751
17	1085.8	46.7	4751	5	HGA238850	Homo sapi	HGA238850	20	1085.8	46.7	4751
18	1085.8	46.7	4751	5	AX211348	Sequence	AX211348				
19	1085.8	46.7	4751	5	AX2211348	Sequence	AX2211348				
20	1085.8	46.7	4751	5	AX2211348	Sequence	AX2211348				

181 TCCCTTCGGGTGTTTCGGCAGCCACAAAGCAGTGGAAATCGAGCAGGCGGGTGAAGTCA 240
181 TCCCTTCGGGTGTTTCGGCAGCCACAAAGCAGTGGAAATCGAGCAGGCGGGTGAAGTCA 240
241 GCGGGGCCCTGGATCATCCCTCAGCGACTTCGGGTGTTTACGGGACCTGATCATG 300
241 GCGGGGCCCTGGATCATCCCTCAGCGACTTCGGGTGTTTACGGGACCTGATCATG 300
301 CTGCTGCTGATGTGGGGAACCTCATCGTCTCCCTGCTGGGCATCACCTTCTTCAAGGAG 360
301 CTGCTGCTGATGTGGGGAACCTCATCGTCTCCCTGCTGGGCATCACCTTCTTCAAGGAG 360
361 GAGAACTCCCGCCTTGGATCGTCTTCAAGTATGTCTGATATCTTCTTCTCTACTGGAT 420
421 CTGGTGTCAACTTCGGAAGCGGCATCGTGGTGGAGAGGGTCTGAGATCTCTGCTGGCA 480
421 CTGGTGTCAACTTCGGAAGCGGCATCGTGGTGGAGAGGGTCTGAGATCTCTGCTGGCA 480
481 CCGGGGCCATCGCAGCGCTACCTCGGCACATGTTCTCGTTGACCTCATCTCTCTCT 540
481 CCGGGGCCATCGCAGCGCTACCTCGGCACATGTTCTCGTTGACCTCATCTCTCTCTCT 540
541 ATCCCTGTGGATTAATCTTCTTAGTGGAGCTGGAGCCACGGTTGGACGCTGAGGTC 600
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601 TACAAAACGCGCAGCGGCCTACGCTGTTCTGCTTCAACAGATCTTAAGCCTGCTGAGG 660
661 CTGCTCGCCTCTCCCGCCTCATCCGCTACATACACAGTGGAGAGATCTTTACATG 720
661 CTGCTCGCCTCTCCCGCCTCATCCGCTACATACACAGTGGAGAGATCTTTACATG 720
721 ACCTATGACCTGCGCAGTGTGTTGCGATCTTCAACCTCATTTGGGATGATGCTGCTG 780
721 ACCTATGACCTGCGCAGTGTGTTGCGATCTTCAACCTCATTTGGGATGATGCTGCTG 780
781 CTATGTCACTGGATGGCTGTGCAATGCTGGTCCCATGCTGAGGACTTCCCTCCC 840
781 CTATGTCACTGGATGGCTGTGCAATGCTGGTCCCATGCTGAGGACTTCCCTCCC 840
841 GACTGTGGGTCTCCATCAACACATGGTGAACCACTCGTGGGCGCCAGTATTTCCCAT 900
841 GACTGTGGGTCTCCATCAACACATGGTGAACCACTCGTGGGCGCCAGTATTTCCCAT 900
901 GCCCTGTTCAAGGCCATGAGCCACATGCTGTGCAATGGCTATGGGCGAGCAGGCACTGTA 960
901 GCCCTGTTCAAGGCCATGAGCCACATGCTGTGCAATGGCTATGGGCGAGGCACTGTA 960
961 GGCATGCCGAGCTCTGGCTCAGCATGCTGAGTATGATGCTGGTCCCATGCTGACGCC 1020
961 GGCATGCCGAGCTCTGGCTCAGCATGCTGAGTATGATGCTGGTCCCATGCTGACGCC 1020
1021 ATGTTTCATCGGCCATGCCAGGCACATCATCGTCCCTGAGTCTTCCCGGGCTCAGTAC 1080
1021 ATGTTTCATCGGCCATGCCAGGCACATCATCGTCCCTGAGTCTTCCCGGGCTCAGTAC 1080
1081 CAGGAGAAGTACAAGCAGGTGGAGCAGTACATGCTTCCCAAGTGTGCGCAGACACG 1140
1081 CAGGAGAAGTACAAGCAGGTGGAGCAGTACATGCTTCCCAAGTGTGCGCAGACACG 1140
1141 CCGCAGCGCATCAAGTATATGAGCACCGCTACAGGCAAGATGTTCCATGAGGAA 1200
1141 CCGCAGCGCATCAAGTATATGAGCACCGCTACAGGCAAGATGTTCCATGAGGAA 1200
1201 AGCATCTGGGAGCTGAGCGCGCTTCCGAGGAGATCATTAACCTTCACTGTCGG 1260
1201 AGCATCTGGGAGCTGAGCGCGCTTCCGAGGAGATCATTAACCTTCACTGTCGG 1260

1261 GGCCTGTGGGCCACATGCTGCTGTTGCTCCCATGCGCAGCCAGCTTCGTCACTGCACTT 1320
1261 GGCCTGTGGGCCACATGCTGCTGTTGCTCCCATGCGCAGCCAGCTTCGTCACTGCACTT 1320
1321 CTCACCAAGCTGCGCTTTGAGGTCTTCAGCGCGGGGATCTCGTGGTCCGTGAGGCTCC 1380
1321 CTCACCAAGCTGCGCTTTGAGGTCTTCAGCGCGGGGATCTCGTGGTCCGTGAGGCTCC 1380
1381 GTGGGGAGGAAGATGTACTTTCATCCAGCATGGGTGCTCAGTGTGCTGGCCCGCGCGCC 1440
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1441 CCGGACACACGCCCTCACCGATGGATCTTCTTGGGGAGATCTGCTCTCTAACTAGGGGC 1500
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1981 CGAGCTGGCCCATGGGCATCCACCTCCCGCTGCGCCCGCCACCTGCGCCGAACCTTGAC 2040
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2161 CAGCGGCAACAGCGCATGGCTCTCTGGGGCTAAGGGATCAGGAAGTGAAGCTGCT 2220
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2221 CCCTCAGGGCTCTGGGCAAACTCTCAAGGACAGCCCGCCAGCCCGCCAGCCACCACTGCT 2280
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2281 GAGCAGCGCACACCCCGGGGTCTCCAGCTTCTGCCCAACATGTAA 2325
2281 GAGCAGCGCACACCCCGGGGTCTCCAGCTTCTGCCCAACATGTAA 2325

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OM nucleic - nucleic search, using sw model

Run on: June 26, 2006, 22:18:28 ; Search time 1446 Seconds
(without alignments)
11210.565 Million cell updates/sec

Title: US-09-767-597-2
Perfect score: 2325
Sequence: 1 atggagcagacagcggcc.....agcttctgccaacatgtaa 2325

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq 8;
1: Geneseqn1980s.*
2: Geneseqn1990s.*
3: Geneseqn2000s.*
4: Geneseqn2001as.*
5: Geneseqn2001bs.*
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8: Geneseqn2003as.*
9: Geneseqn2003bs.*
10: Geneseqn2003cs.*
11: Geneseqn2003ds.*
12: Geneseqn2004as.*
13: Geneseqn2004bs.*
14: Geneseqn2005s.*
15: Geneseqn2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2325	100.0	2325	3 AAC66779	AAC66779 Human hyp
2	2323.4	99.9	2325	8 ABZ75841	ABZ75841 Human HCN
3	2323.4	99.9	2325	8 ABZ58682	ABZ58682 Human HCN
4	2323.4	99.9	2325	8 ACA61916	ACA61916 cDNA enco
5	2323.4	99.9	2325	10 ABX95515	ABX95515 cDNA enco
6	2323.4	99.9	2325	14 AEB12299	AEB12299 Human HCN
7	2320.6	99.8	2340	6 ABK86387	ABK86387 Human HCN
8	2320.6	99.8	2340	6 ABK86386	ABK86386 Human HCN
9	2320.2	99.8	3852	6 AAL44691	AAL44691 Human tra
10	2319	99.7	2340	6 ABK86385	ABK86385 Human HCN
11	2215.4	95.3	3601	12 ADQ83229	ADQ83229 Human tum
12	2215.4	95.3	3601	13 ADQ85140	ADQ85140 Human tum
13	2122.6	91.3	2217	8 ABX71090	ABX71090 Novel hum
14	2115.4	91.0	3209	13 ACN43221	ACN43221 Human dia
15	2110.4	90.8	3496	6 AAD29758	AAZ29758 Human hyp
16	2110.4	82.2	3438	3 AAG62050	AAG62050 Hydropob
17	1876.2	80.7	2340	14 AEB12318	AEB12318 Mouse HCN
18	1872.8	80.6	2343	14 AEB12314	AEB12314 Rat HCN3

19	1810.4	77.9	1812	14 AEB12323	AEB12323 Human HCN
20	1721.8	74.1	3567	12 ADH22603	ADH22603 cDNA enco
21	1087.4	46.8	4751	2 AAZ09496	AAZ09496 Human hea
22	1085.8	46.7	4751	6 AEB12300	AEB12300 Human HCN
23	1085.8	46.7	4751	6 AAD29757	AAZ29757 Human hyp
24	1085.8	46.7	5065	4 AAH48730	AAH48730 Human HCN
25	1085.8	46.7	5065	13 ADR86593	ADR86593 Human HCN
26	1085.8	46.7	5499	4 ABA09197	ABA09197 Human cat
27	1073.2	46.2	3597	14 AEB12315	AEB12315 Rat HCN4
28	1061.6	45.7	2214	14 AEB12324	AEB12324 Human HCN
29	1061.6	45.7	2256	14 AEB12325	AEB12325 Human HCN
30	1054	45.3	3606	14 AEB12319	AEB12319 Mouse HCN
31	1045.4	45.0	3372	4 AAH48729	AAH48729 Human HCN
32	1045.4	45.0	3372	13 ADQ83419	ADQ83419 Human tum
33	1043.8	44.9	2670	14 AEB12298	AEB12298 Human HCN
34	1043.8	44.9	3459	6 AAD29756	AAZ29756 Human hyp
35	1043.4	44.9	2160	14 AEB12322	AEB12322 Human HCN
36	1019.2	43.8	2871	14 AEB12313	AEB12313 Rat HCN2
37	1016.2	43.7	1790	2 AAX84445	AAX84445 Human bra
38	1012.6	43.6	1820	2 AAZ09488	AAZ09488 Bovine re
39	1007.8	43.3	2886	2 AAZ09491	AAZ09491 Human Ih
40	1006.4	43.3	2592	14 AEB12317	AEB12317 Mouse HCN
41	1006.4	43.3	3102	4 AAH48731	AAH48731 Murine HC
42	983.8	42.3	2125	10 ADC87558	ADC87558 Human GPC
43	980.6	42.2	1584	2 AAX84444	AAX84444 Mouse bra
44	928.2	39.9	3431	4 AAH98302	AAH98302 Human EST
45	880	37.8	2817	14 AEB12321	AEB12321 Rainbow t

ALIGNMENTS

RESULT 1
AAC66779
ID AAC66779 standard; cDNA; 2325 BP.

XX AAC66779;

DT 16-FEB-2001 (first entry)

XX Human hyperpolarisation-activated channel HAC3 coding sequence.

XX Human; hyperpolarisation-activated channel; HAC3; neuroleptic; nontropic;
cerebroprotective; antimigraine; antiarrhythmic; gene therapy;
pacemaker dysfunction; familial sinus rhythm disease;
sick sinus syndrome associated with atrial fibrillation;
sinus tachycardia; bradycardia; ventricular arrhythmia; bipolar disease;
schizophrenia; central nervous system disorder; migraine; seizure;
stroke; ss.

XX Homo sapiens.

XX Key Location/Qualifiers
FH 1..2325
FT /*tag= a
FT /product= "Human HAC3"

XX WO2000063349-A1.

XX 26-OCT-2000.

XX 13-APR-2000; 2000WO-US009865.

XX 15-APR-1999; 99US-0129456P.

XX (ICAG-) ICAGEN INC.

XX Jegla TJ;

XX WPI; 2000-679592/66.

XX P-PSDB; AAB28375.

XX Novel human hyperpolarization activated channel 3 polypeptide useful to

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OM nucleic - nucleic search, using sw model

Run on: June 26, 2006, 23:05:18 ; Search time 10971 Seconds
(without alignments)
11850.556 Million cell updates/sec

Title: US-09-767-597-2
Perfect score: 2325
Sequence: 1 atggagcagagcagcgcc.....agttctctgccaacatgtaa 2325

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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2: gb_est3.*
3: gb_est4.*
4: gb_est5.*
5: gb_est6.*
6: gb_est7.*
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9: gb_est8.*
10: gb_est9.*
11: gb_gss1.*
12: gb_gss2.*
13: gb_gss3.*
14: gb_gss4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1876.2	80.7	3265	6 AK032225	Mus muscu
2	1803.6	77.6	4015	6 AK082719	Mus muscu
3	1619	69.6	1620	14 AY399924	AY399924 Homo sapi
4	1315.8	56.6	1638	14 AY399926	AY399926 Mus muscu
5	1292.2	55.6	1620	14 AY399925	AY399925 Pan trogl
6	1045	44.9	1794	6 BC033619	BC033619 Homo sapi
7	875.2	37.6	1725	14 DQ051256	DQ051256 Homo sapi
8	840.4	36.1	1689	14 DQ051257	DQ051257 Pan trogl
9	747.2	32.1	1087	7 BE798933	BE798933 601583714
10	723.6	31.1	912	5 CD513082	CD513082 AGNCOURT
11	716.2	30.8	858	7 BE793179	BE793179 601581483
12	682.2	29.3	963	2 B1117045	B1117045 602867826
13	673.6	29.0	815	8 CV675880	CV675880 i148a08.k
14	667.4	28.7	692	2 BE7918260	BE7918260 60182933
15	637.4	27.0	771	9 DR000745	DR000745 TC122071
16	607	26.1	780	7 BE260963	BE260963 601151693
17	600.2	25.8	605	8 CV030457	CV030457 9582 Full
18	594	25.5	810	10 DR762372	DR762372 HBSC4_139
19	587.4	25.3	776	8 CV107914	CV107914 AGNCOURT

20	595	25.2	785	8	CN528592	CN528592	UT-M-HQ0-
21	582.4	25.0	1121	10	DM602851	DM602851	CGX162-E0
22	577.4	24.8	965	2	BI490063	BI490063	603031868
23	568.6	24.5	811	10	DV880381	DV880381	LB02613.C
24	565.4	24.3	567	9	DA169687	DA169687	DA169687
25	565.4	24.3	954	4	CB201579	CB201579	AGNCOURT
26	564.4	24.3	566	9	DA522053	DA522053	DA522053
27	563	24.2	565	9	DA770024	DA770024	DA770024
28	559.4	24.1	677	9	DR005083	DR005083	TC121938
29	557.4	24.0	559	9	DA811505	DA811505	DA811505
30	551.4	23.7	554	9	DA414799	DA414799	DA414799
31	546.4	23.5	548	9	DA626265	DA626265	DA626265
32	540	23.2	562	9	DA523993	DA523993	DA523993
33	539.2	23.2	728	3	BM944254	BM944254	UT-M-EHOP
34	536.8	23.1	635	9	DR003598	DR003598	TC122041
35	526.4	22.6	913	4	CA488537	CA488537	AGNCOURT
36	524.6	22.6	717	5	CK599046	CK599046	AGNCOURT
37	524	22.5	852	2	BI752028	BI752028	603022143
38	519.6	22.3	786	2	BG974320	BG974320	602844071
39	504	21.7	881	2	BG298718	BG298718	602396636
40	495.4	21.3	1030	3	BQ070889	BQ070889	AGNCOURT
41	494.4	21.3	496	9	DB169730	DB169730	DB169730
42	491	21.1	590	9	DA722534	DA722534	DA722534
43	484.2	20.8	800	10	DV882949	DV882949	LB02625.C
44	484	20.8	592	9	DA809823	DA809823	DA809823
45	480.4	20.7	895	4	CA488767	CA488767	AGNCOURT

ALIGNMENTS

RESULT 1	AK032225	3265 bp	mRNA	linear	HTC 02-SEP-2005
LOCUS	Mus musculus adult male olfactory brain cDNA, RIKEN full-length				
DEFINITION	enriched library, clone:6430507E23				
	product:hyperpolarization-activated, cyclic nucleotide-gated K+ 3,				
	full insert sequence.				
ACCESSION	AK032225				
VERSION	AK032225.1	GI:26328056			
KEYWORDS	HTC; CAP trapper.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;				
	Sciurognathi; Muridea; Muridae; Murinae; Mus.				
REFERENCE	1				
AUTHORS	Carninci, P. and Hayashizaki, Y.				
TITLE	High-efficiency full-length cDNA cloning				
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)				
PUBMED	10349636				
REFERENCE	2				
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,				
	Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.				
	Normalization and subtraction of cap-trapper-selected cDNAs to				
	prepare full-length cDNA libraries for rapid discovery of new genes				
	Genome Res. 10 (10), 1617-1630 (2000)				
	11042159				
REFERENCE	3				
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,				
	Konno, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M.,				
	Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,				
	Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,				
	Fujitake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,				
	Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,				
	Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.				
	RIKEN integrated sequence analysis (RISA) system--384-format				
	sequencing pipeline with 384 multicapillary sequencer				
	Genome Res. 10 (11), 1757-1771 (2000)				
	11076861				
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format				
JOURNAL	sequencing pipeline with 384 multicapillary sequencer				
PUBMED	Genome Res. 10 (11), 1757-1771 (2000)				
REFERENCE	4				
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the				
	FANTOM Consortium.				

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OM nucleic - nucleic search, using sw model

Run on: June 26, 2006, 23:05:14 ; Search time 438 Seconds
(without alignments)
9932.256 Million cell updates/sec

Title: US-09-767-597-2

Perfect score: 2325

Sequence: 1 atggaggagcagcgccgccc.....agcttttcgcaacatgtaa 2325

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents:NA:

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- 2: /EMC Celerera SIDS3/ptodata/2/ina/5 COMB.seq.*
- 3: /EMC Celerera SIDS3/ptodata/2/ina/6A COMB.seq.*
- 4: /EMC Celerera SIDS3/ptodata/2/ina/6B COMB.seq.*
- 5: /EMC Celerera SIDS3/ptodata/2/ina/7 COMB.seq.*
- 6: /EMC Celerera SIDS3/ptodata/2/ina/H COMB.seq.*
- 7: /EMC Celerera SIDS3/ptodata/2/ina/PTUS COMB.seq.*
- 8: /EMC Celerera SIDS3/ptodata/2/ina/PP COMB.seq.*
- 9: /EMC Celerera SIDS3/ptodata/2/ina/RE COMB.seq.*
- 10: /EMC Celerera SIDS3/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	2122.6	91.3	2976	US-09-774-528-317 Sequence 317, App
2	2122.6	91.3	2976	US-10-120-988-317 Sequence 317, App
3	1085.8	46.7	4276	US-09-949-016-4900 Sequence 4900, Ap
4	1085.8	46.7	5065	US-09-949-016-744 Sequence 744, App
5	1085.8	46.7	5065	US-10-067-457-4 Sequence 4, Appli
6	1047	45.0	3235	US-09-949-016-1392 Sequence 1392, Ap
7	1045.4	45.0	3372	US-09-949-016-165 Sequence 165, App
8	1045.4	45.0	3372	US-10-067-457-2 Sequence 2, Appli
9	1038.2	44.7	1792	US-09-086-436-40 Sequence 40, Appl
10	1016.2	43.7	1790	US-08-997-685A-11 Sequence 11, Appl
11	1006.4	43.3	3102	US-10-067-457-6 Sequence 6, Appli
12	983.8	42.3	1512	US-09-086-436-32 Sequence 32, Appl
13	980.6	42.2	1584	US-08-997-685A-3 Sequence 3, Appli
14	935.8	40.2	1518	US-09-086-436-34 Sequence 34, Appl
15	871.2	37.5	1507	US-09-997-685A-5 Sequence 5, Appli
16	844.6	36.3	1307	US-09-172-423-3 Sequence 3, Appli
17	825.8	35.5	2733	US-08-997-685A-1 Sequence 1, Appli
18	784.2	33.7	3224	US-09-774-528-238 Sequence 238, App
19	784.2	33.7	3224	US-10-120-988-238 Sequence 238, App
20	740.4	31.8	2246	US-09-086-436-38 Sequence 38, Appl
21	740.4	31.8	2263	US-08-997-685A-9 Sequence 9, Appli
22	328.6	14.1	1083	US-09-270-767-1038 Sequence 1038, Ap
23	328.6	14.1	1083	US-09-270-767-16320 Sequence 16320, A

c	24	314.8	13.5	13011	2	US-08-791-849A-14	Sequence 14, Appl
	25	265.4	11.4	31467	3	US-09-949-016-13134	Sequence 13134, A
	26	265.4	11.4	31868	3	US-09-949-016-11907	Sequence 11907, A
	27	239.4	11.2	50453	3	US-09-949-016-16642	Sequence 16642, A
	28	259.4	11.2	51242	3	US-09-949-016-12486	Sequence 12486, A
	29	176.4	7.6	601	3	US-09-949-016-32298	Sequence 32298, A
	30	176.4	7.6	601	3	US-09-949-016-173035	Sequence 173035, A
	31	166	7.1	15108	3	US-09-949-016-11786	Sequence 11786, A
	32	166	7.1	15108	3	US-09-949-016-17205	Sequence 17205, A
	33	163.6	7.0	601	3	US-09-949-016-21135	Sequence 21135, A
	34	163.6	7.0	601	3	US-09-949-016-47503	Sequence 47503, A
	35	163.2	7.0	601	3	US-09-949-016-21136	Sequence 21136, A
	36	163.2	7.0	601	3	US-09-949-016-47504	Sequence 47504, A
	37	134	5.8	1040	3	US-08-086-436-36	Sequence 36, Appl
	38	129.2	5.6	601	3	US-09-949-016-21121	Sequence 21121, A
	39	129.2	5.6	601	3	US-09-949-016-47489	Sequence 47489, A
	40	122	5.2	1060	3	US-08-997-685A-7	Sequence 7, Appli
	41	120.6	5.2	601	3	US-09-949-016-21142	Sequence 21142, A
	42	120.6	5.2	601	3	US-09-949-016-47510	Sequence 47510, A
	43	117.8	5.1	601	3	US-09-949-016-21134	Sequence 21134, A
	44	117.8	5.1	601	3	US-09-949-016-47502	Sequence 47502, A
	45	107.2	4.6	601	3	US-09-949-016-21141	Sequence 21141, A

ALIGNMENTS

RESULT 1
US-09-774-528-317
; Sequence 317, Application US/09774528
; Patent No. 6743619
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyuan
; APPLICANT: Zhang, Jie
; APPLICANT: Zhao, Qing A.
; APPLICANT: Yang, Yonghong
; APPLICANT: Xue, Aidong J.
; APPLICANT: Wehrman, Tom
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Wang, Dunrui
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6743619el Nucleic Acids and
; FILE REFERENCE: 802
; CURRENT APPLICATION NUMBER: US/09/774,528
; CURRENT FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 441
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 317
; LENGTH: 2976
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (18)..(2174)
US-09-774-528-317

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						Gaps	0;
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Qy	257	TCCACCCCTACAGCAGCTTCGGGTTTTTACTGGGACCTGATCATCTGCTGCTGATGGTGG	316				
Db	106	TCCACCCCTACAGCAGCTTCGGGTTTTTACTGGGACCTGATCATCTGCTGCTGATGGTGG	165				

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301 CTGCTGCTGATGTTGGGGAACCTCATGTCCTGCTGCTGGGACATCACTTCITCAAGGAG 360
361 GAGAACTCCCGCTTGGATCGCTTCAACGTAATGTCGATATCTTCTTCTTCTTCTTCTTCT 420
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421 CTGGTGTCTCAATTCGGAACCGGCATCGTGGTGGAGGAGGTCTGAGATCTCTGTGGCA 480
421 CTGGTGTCTCAATTCGGAACCGGCATCGTGGTGGAGGAGGTCTGAGATCTCTGTGGCA 480
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901 GCCTGTTCAGGCCATGAGCCACATGCTGTGCAATTTGGCTATGGGCGAGCAGCACTGTA 960
961 GGCAATCCCGACGTCTGGCTCACCATGCTCAGCATGATCGTAGGTGCCACATGCTACGCC 1020
961 GGCAATCCCGACGTCTGGCTCACCATGCTCAGCATGATCGTAGGTGCCACATGCTACGCC 1020
1021 ATGTTTCATCGGCCATGCGCAGGACATCATCAGTCCCTGGAATCTTCCCGGGGTGATGAC 1080
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1081 CAGGAGAAGTACAAAGCAGGTGGAGCAGTACATGCTCTCCCAAGCTGCGCAGCAGCAGC 1140
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1141 CCGCAGCGCATCCACAGTACTATGAGCACCGCTACCGGCAAGATGTTTCGATGAGGAA 1200
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1501 CCGGACACACGCTTCTCGGCTGACACCTACTGCGGCTTTACTCACTCAGCGTGGAC 1560
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1561 CATTTCAATGCTGTGCTTGGAGGTTCCTCCATGATGCGCGGGCTTTGAGACTGTGGCC 1620
1561 CATTTCAATGCTGTGCTTGGAGGTTCCTCCATGATGCGCGGGCTTTGAGACTGTGGCC 1620
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1981 CGAGTGGCCCATGGGATCCACCTCCGCGCTGCGCCCACTGCGCCCACTGCGCCCACTG 2040
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2041 GCCAGCTTATCCCGGCGAGGCGCTCCAGGTCTCCCTGCTGGGTCCCTCCAGGAGGA 2100
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2161 CAGCGGCAACAGCGGATGGCTCTCTGGGCGTAAGGATCAGGAAGTGAAGCGGCTGCT 2220
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		Match	Length			
1	2325	100.0	2325	3	US-09-548-933-2	Sequence 2, Appli
2	2323.4	99.9	2325	6	US-10-158-684-9	Sequence 9, Appli
3	2323.4	99.9	2325	6	US-10-158-711-9	Sequence 9, Appli
4	2320.2	99.9	3852	4	US-10-332-447-57	Sequence 57, Appl
5	2122.6	91.3	2976	7	US-10-120-988-317	Sequence 317, App
6	2110.4	90.8	3496	8	US-10-311-795-7	Sequence 7, Appli
7	1085.8	46.7	4751	8	US-10-311-795-5	Sequence 5, Appli
8	1085.8	46.7	5065	6	US-10-067-457-4	Sequence 4, Appli
9	1085.8	46.7	5499	8	US-10-276-774-973	Sequence 973, App
10	1045.4	45.0	3372	6	US-10-067-457-2	Sequence 2, Appli
11	1043.8	44.9	3459	8	US-10-311-795-3	Sequence 3, Appli
12	1043.8	44.9	3459	10	US-10-756-149-1720	Sequence 1720, Ap
13	1038.2	44.7	1792	3	US-09-086-436-40	Sequence 40, Appl
14	1038.2	44.7	1792	3	US-10-753-991-40	Sequence 40, Appl
15	1016.2	43.7	1790	9	US-10-384-107-11	Sequence 11, Appl
16	1006.4	43.3	3102	6	US-10-067-457-6	Sequence 6, Appli
17	988	42.5	1366	7	US-10-017-161-2369	Sequence 2369, Ap

SUMMARIES

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; FEATURE:
; OTHER INFORMATION: human hyperpolarization-activated voltage-gated
; OTHER INFORMATION: cation channel 3 (HAC3)
US-09-548-933-2

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	Query Match	100.0%;	Score 2325;	DB 3;	Length 2325;
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Qy	61	GCGGTGCCCTCCCGTTGCTCCCGCGCTCGACCGCGGCCTCAGGTCGGATCCCGCAATCT	120		
Db	61	GCGGTGCCCTCCCGTTGCTCCCGCGCTCGACCGCGGCCTCAGGTCGGATCCCGCAATCT	120		
Qy	121	GGGCGCTGAGCCTAAGAGGAGGCACCTTTGGAGCGCTGCTCCAGCGCTACAGGATTC	180		
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 1724 GCTTTCATATCCGCGGCTCTCGAGAGCATCACACGAGCGGCGCGCTTCCGGCTT 1783
 1455 CACCGATGATCTTCTTGGGAGATCTGCCT 1487
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RESULT 2

US-11-302-678-27
 ; Sequence 27, Application US/11302678
 ; Publication No. US2006008881A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Millennium Pharmaceuticals, Inc.
 ; APPLICANT: Silos-Santiago, Immaculada
 ; APPLICANT: Venkateswarlu, Karicheti
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
 ; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1435, 559, 34021, 44099, 25278,
 ; TITLE OF INVENTION: 641, 260, 55089, 21407, 42032, 46556, 62553, 302, 323,
 ; TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.
 ; FILE REFERENCE: MPI02-012PIRNM OMNI
 ; CURRENT APPLICATION NUMBER: US/11/302,678
 ; CURRENT FILING DATE: 2005-12-14
 ; PRIOR APPLICATION NUMBER: US/10/345,680
 ; PRIOR FILING DATE: 2003-01-16
 ; PRIOR APPLICATION NUMBER: US 60/349,511
 ; PRIOR FILING DATE: 2002-01-18
 ; PRIOR APPLICATION NUMBER: US 60/360,500
 ; PRIOR FILING DATE: 2002-02-28
 ; PRIOR APPLICATION NUMBER: US 60/365,041
 ; PRIOR FILING DATE: 2002-03-15
 ; PRIOR APPLICATION NUMBER: US 60/374,063
 ; PRIOR FILING DATE: 2002-04-19
 ; PRIOR APPLICATION NUMBER: US 60/403,468
 ; PRIOR FILING DATE: 2002-08-14
 ; PRIOR APPLICATION NUMBER: US 60/414,262
 ; PRIOR FILING DATE: 2002-09-27
 ; PRIOR APPLICATION NUMBER: US 60/419,986
 ; PRIOR FILING DATE: 2002-10-21
 ; PRIOR APPLICATION NUMBER: US 60/423,809
 ; PRIOR FILING DATE: 2002-11-05
 ; PRIOR APPLICATION NUMBER: US 60/429,797
 ; PRIOR FILING DATE: 2002-11-26
 ; NUMBER OF SEQ ID NOS: 66
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 27
 ; LENGTH: 2085
 ; TYPE: DNA
 ; ORGANISM: Homo Sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)...(2085)

US-11-302-678-27
 Query Match 2.9%; Score 68.4; DB 7; Length 2085;
 Best Local Similarity 47.8%; Pred. No. 1.7e-06;
 Matches 266; Conservative 0; Mismatches 281; Indels 9; Gaps 2;
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 QY 1053 GTCCCTGAGCTCTTCCCGGCGTCAGTACAGGAGAAAGTAAAGCAGGTGGAGAGTACAT 1112
 DB 1212 GAATATGAATGCCCTACCGGCGAGAGTTCCAGGCCAAGATTGATTCATCAAGCAGTACAT 1271
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 DB 1272 GAGTTCGCAAGGTTCACCAAGGACTTGGAGACCGGGTTATCCGGTGGTTTACTACTT 1331
 QY 1173 CTA---CCAGGGCAAGATGTTTCGATGAGGAAAGCATCTCGGGCGAGCTGAGCGAGCGCT 1229
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 QY 1230 TCGGAGAGATCAATTAATCTTCACTGTGCGGGCGCTGCTGCGGCCACATGCGCTGTTTGC 1289
 DB 1392 GAAGGCTGAGATCGCCATCAACGTCACCTGACACGCTGAAGAGGTTCGCATCTTCCA 1451
 QY 1290 CCATCGGACCCAGCTTCGTCAGTCTTCCACCAAGCTGCGCTTTGAGTCTTCCA 1349
 DB 1452 GGACTGTGAGGAGGCTGCTGGTGGAGCTGGTGAAGCTGCGACCCACTGTGTTGAG 1511
 QY 1350 GCCGGGGATCTCGTGTGCTGAGGGTCCGTGGGAGGAGATGTACTTTCATCCAGCA 1409
 DB 1512 CCCTGGGATATATCTCAAGAGGAGATATTTGGGAGGAGATGTACTATCATCAACGA 1571
 QY 1410 TGGGCTGCTAGTGTGCTGGC-----CCGCGGCGCCCGGAGACACACGCCCTCACCGATGG 1463
 DB 1572 GGGCAAGCTGGCGCTGCTGATGATGGGTGCTGATGATGATGATGATGATGATGATGATGAT 1631
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RESULT 3

US-11-302-678-25
 ; Sequence 25, Application US/11302678
 ; Publication No. US2006008881A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Millennium Pharmaceuticals, Inc.
 ; APPLICANT: Silos-Santiago, Immaculada
 ; APPLICANT: Venkateswarlu, Karicheti
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
 ; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1435, 559, 34021, 44099, 25278,
 ; TITLE OF INVENTION: 641, 260, 55089, 21407, 42032, 46556, 62553, 302, 323,
 ; TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.
 ; FILE REFERENCE: MPI02-012PIRNM OMNI
 ; CURRENT APPLICATION NUMBER: US/11/302,678
 ; CURRENT FILING DATE: 2005-12-14
 ; PRIOR APPLICATION NUMBER: US/10/345,680
 ; PRIOR FILING DATE: 2003-01-16
 ; PRIOR APPLICATION NUMBER: US 60/349,511
 ; PRIOR FILING DATE: 2002-01-18
 ; PRIOR APPLICATION NUMBER: US 60/360,500
 ; PRIOR FILING DATE: 2002-02-28
 ; PRIOR APPLICATION NUMBER: US 60/365,041
 ; PRIOR FILING DATE: 2002-03-15
 ; PRIOR APPLICATION NUMBER: US 60/374,063
 ; PRIOR FILING DATE: 2002-04-19
 ; PRIOR APPLICATION NUMBER: US 60/403,468

GenCore version 5.1.9
 Copyright (c) 1993 - 2006 Bioceleration Ltd.
 OM nucleic - nucleic search, using sw model
 Run on: June 26, 2006, 23:15:26 ; Search time 90 Seconds
 (without alignments)
 6192.891 Million cell updates/sec
 Title: US-09-767-597-2
 Perfect score: 2325
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 Gapop 10.0 , Gapext 1.0
 Searched: 296510 seqs, 119862409 residues
 Total number of hits satisfying chosen parameters: 593020

Minimum DB seq length: 0
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 Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries
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 Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	77.8	3.3	2544	6	US-10-449-902-18848
2	68.4	2.9	2085	7	US-11-302-678-27
3	68.4	2.9	3486	7	US-11-302-678-25
4	57.2	2.5	3083	7	US-11-312-958-29
5	56.4	2.4	2326	6	US-10-449-902-17165
6	55.8	2.4	1580	6	US-10-449-902-2520
7	48.8	2.1	2439	6	US-10-449-902-25641
8	48.4	2.1	152331	7	US-11-175-714-86
9	48.2	2.1	1320	6	US-10-449-902-19536
10	48	2.1	2064	6	US-10-449-902-9081
11	45.8	2.0	17203	6	US-10-517-441-121
12	45.6	2.0	1222	6	US-10-449-902-25996
13	45.2	1.9	128361	6	US-10-505-928-151
14	44.2	1.9	1184	6	US-10-449-902-11798
15	44.2	1.9	2745	6	US-10-449-902-20146
16	44.2	1.9	3553	7	US-11-312-958-17
17	44	1.9	1304	6	US-10-449-902-28022
18	43.8	1.9	2410	6	US-10-449-902-24550
19	43.6	1.9	1679	6	US-10-449-902-10109
20	43	1.8	11978	7	US-11-257-851A-63
21	42.8	1.8	4001	6	US-10-517-441-132
22	42.8	1.8	84428	7	US-11-330-363-1
23	42.6	1.8	1787	6	US-10-449-902-25521
24	42.2	1.8	580	6	US-10-953-349-27203
25	42.2	1.8	1441	6	US-10-953-349-28919

26	42	1.8	2092	6	US-10-449-902-19116	Sequence 19116, A
27	41.6	1.8	1480	6	US-10-449-902-16130	Sequence 16130, A
28	40.8	1.8	1123	6	US-10-449-902-23368	Sequence 23368, A
29	40.8	1.8	1256	6	US-10-449-902-8986	Sequence 8986, Ap
30	40.6	1.7	3580	7	US-11-289-102-32	Sequence 32, Appl
31	40.4	1.7	1986	6	US-10-449-902-6333	Sequence 6333, Ap
32	40.2	1.7	1317	6	US-10-449-902-24565	Sequence 24565, A
33	40.2	1.7	2796	6	US-10-449-902-19530	Sequence 19530, A
34	40	1.7	955	6	US-10-953-349-23686	Sequence 23686, A
35	40	1.7	1419	6	US-10-449-902-10331	Sequence 10331, A
36	40	1.7	1559	6	US-10-449-902-22528	Sequence 22528, A
37	40	1.7	1590	6	US-10-449-902-1559	Sequence 1559, Ap
38	40	1.7	1598	6	US-10-449-902-8452	Sequence 8452, Ap
39	40	1.7	1704	6	US-10-449-902-17171	Sequence 17171, A
40	40	1.7	2173	6	US-10-449-902-22156	Sequence 22156, A
41	40	1.7	2266	6	US-10-449-902-20171	Sequence 20171, A
42	40	1.7	2798	6	US-10-449-902-26902	Sequence 26902, A
43	39.8	1.7	1291	6	US-10-449-902-6445	Sequence 6445, Ap
44	39.6	1.7	1533	6	US-10-449-902-2853	Sequence 2853, Ap
45	39.6	1.7	2057	6	US-10-449-902-17942	Sequence 17942, A

ALIGNMENTS

RESULT 1
 US-10-449-902-18848
 ; Sequence 18848, Application US/10449902
 ; Publication NO. US20060123505A1
 ; GENERAL INFORMATION:
 ; APPLICANT: National Institute of Agrobiological Sciences
 ; APPLICANT: Bio-oriented Technology Research Advancement Institution.
 ; APPLICANT: The Institute of Physical and Chemical Research.
 ; APPLICANT: Foundation for Advancement of International Research.
 ; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
 ; FILE REFERENCE: MOA-A0205V1-US
 ; CURRENT APPLICATION NUMBER: US/10/449,902
 ; CURRENT FILING DATE: 2003-05-29
 ; PRIOR APPLICATION NUMBER: JP 2002-203269
 ; PRIOR FILING DATE: 2002-05-30
 ; PRIOR APPLICATION NUMBER: JP 2002-383870
 ; PRIOR FILING DATE: 2002-12-11
 ; NUMBER OF SEQ ID NOS: 56791
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 18848
 ; LENGTH: 2544
 ; TYPE: DNA
 ; ORGANISM: Oryza sativa
 ; PUBLICATION INFORMATION:
 ; DATABASE ACCESSION NUMBER: AK069229
 ; DATABASE ENTRY DATE: 2001-12-06
 US-10-449-902-18848

Query Match	3.3%;	Score	77.8;	DB	6;	Length	2544;		
Best Local Similarity	46.3%;	Pred. No.	1.5e-08;						
Matches	293;	Conservative	0;	Mismatches	337;	Indels	3;	Gaps	1;
QY	858	CAACACATGGTGAACCACTCGTGGGGCCGACAGTATTC	917						
Db	1184	CGAGTCATCAAGTCAAAGACTTCACCTCCAAGCTCTCTACTGCTCTGTGGGGCCT	1243						
QY	918	GAGCCACATGCTGTGATTTGGCTATGGCAGCAGGACCTGTAGGCATGCCGACGTCGTG	977						
Db	1244	TGCCAACCTCAGCACGCTGGGCAAGGGCTGCAGACGAGCATATACACGGGGAGGCGCT	1303						
QY	978	GCTCACCATGCTCAGCATGATCGTAGGTGCCACATGCTACGCCATGTTTCATGGCCATGC	1037						
Db	1304	GTTCGATATTCCTGGGACGTTTCGGGCTGATCTCTGATGGCGATGCTGATCGGCAACAT	1363						
QY	1038	CACGGCACTCATCCAGTCCCTGACTCTTCCCGGCGTCAGTACCGAGGAAGTACAAGCA	1097						
Db	1364	CCAGCGTACCTGCAGTCGATGACCGTGGGCTGAGGAGATCGGGTGACGGGGCGCA	1423						

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 26, 2006, 20:17:52 ; Search time 201 Seconds
(without alignments)
1760.624 Million cell updates/sec

Title: US-09-767-597-1
Perfect score: 4038
Sequence: 1 MEABQRPAGASGATPGLE.....PRPPVPEPATPRGLQLSANM 774

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing First 45 summaries

Database : A Geneseq 8.*

- 1: Geneseqp1980s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*
- 9: Geneseqp2005s.*
- 10: Geneseqp2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4038	100.0	774	3 AAB28375	AAB28375 Human hyp
2	4038	100.0	774	5 AAO14208	AAO14208 Human tra
3	4038	100.0	774	6 ABU09681	ABU09681 Human HCN
4	4038	100.0	774	6 ABP71446	ABP71446 Human HCN
5	4038	100.0	774	6 ABP71038	ABP71038 Human HCN
6	4038	100.0	774	6 ABU10228	ABU10228 Human HCN
7	4028	99.8	774	6 AAU99980	AAU99980 Human HCN
8	4026	99.7	774	5 AAU99979	AAU99979 Human HCN
9	4022	99.6	774	5 AAU99978	AAU99978 Human HCN
10	3837.5	95.0	741	8 ABM84569	ABM84569 Human dia
11	3670	90.9	703	5 AAE18678	AAE18678 Human hyp
12	2540	62.9	1203	4 AAB86462	AAB86462 Human HCN
13	2540	62.9	1203	5 AAE18677	AAE18677 Human hyp
14	2540	62.9	1203	5 ADR86636	ADR86636 Human HCN
15	2540	62.9	1245	4 ABB11953	ABB11953 Human cat
16	2402	59.5	889	4 AAB86461	AAB86461 Human HCN
17	2402	59.5	889	4 AAE18676	AAE18676 Human hyp
18	2402	59.5	889	9 AEA17266	AEA17266 Murine cyc
19	2391.5	59.2	863	4 AAB86463	AAB86463 Human HCN
20	2350	58.2	882	5 AAE21167	AAE21167 Human TRI
21	2346	58.1	882	8 ADR44920	ADR44920 Polypepti
22	2346	58.1	890	5 AAU11712	AAU11712 Human HCN
23	2346	58.1	890	6 ABU09680	ABU09680 Human HCN

24	2346	58.1	890	6 ABP71445	ABP71445 Human HCN
25	2346	58.1	890	6 ABP71037	ABP71037 Human HCN
26	2346	58.1	890	6 ABU10227	ABU10227 Human HCN
27	2346	58.1	890	7 ADJ95124	ADJ95124 Novel NOV
28	2345	58.1	837	5 ABJ10804	ABJ10804 Rabbit HC
29	2344	58.0	890	5 ABJ10800	ABJ10800 Human HCN
30	2341	58.0	890	5 ABJ10797	ABJ10797 Human HCN
31	2341	58.0	890	5 AAU11714	AAU11714 Human ful
32	2340	57.9	890	5 ABJ10799	ABJ10799 Human HCN
33	2340	57.9	890	5 ABJ10801	ABJ10801 Human HCN
34	2340	57.9	890	5 ABJ10793	ABJ10793 Human HCN
35	2333	57.8	890	5 ABJ10798	ABJ10798 Human HCN
36	2333	57.8	890	5 ABJ10796	ABJ10796 Human HCN
37	2332	57.8	890	5 ABJ10794	ABJ10794 Human HCN
38	2329	57.7	890	5 ABJ10795	ABJ10795 Human HCN
39	2325.5	57.6	827	5 AAU11711	AAU11711 Human HCN
40	2321.5	57.5	827	5 AAU11713	AAU11713 Human ful
41	2317	57.4	910	5 ABJ10802	ABJ10802 Mouse bra
42	2316	57.4	910	2 AAY22191	AAY22191 Mouse bra
43	2316	57.4	910	5 ABJ10803	ABJ10803 Rat HCN1
44	2314	57.3	890	5 AAE18675	AAE18675 Human hyp
45	2298	56.9	898	5 ABJ10805	ABJ10805 Consensus

ALIGNMENTS

RESULT 1
AAB28375
ID AAB28375 standard; protein; 774 AA.
XX
AC AAB28375;
XX
DT 16-FEB-2001 (first entry)
XX
DE Human hyperpolarisation-activated channel HAC3.
XX
KW Human; hyperpolarisation-activated channel; HAC3; neuroleptic; nootropic;
cerebroprotective; antimigraine; antiarrhythmic; gene therapy;
pacemaker dysfunction; familial sinus rhythm disease;
sick sinus syndrome associated with atrial fibrillation;
sinus tachycardia; bradycardia; ventricular arrhythmia; bipolar disease;
schizophrenia; central nervous system disorder; migraine; seizure;
stroke.
XX
OS Homo sapiens.
XX
PN WO200063349-A1.
XX
PD 26-OCT-2000.
XX
PF 13-APR-2000; 2000WO-US009865.
XX
PR 15-APR-1999; 99US-0129456P.
XX
PA (ICAG-) ICAGEN INC.
XX
PI Jegla TJ;
XX
DR WPI; 2000-679592/66.
XX
N-PSDB; AAC66779.
XX
PT Novel human hyperpolarization activated channel 3 polypeptide useful to
identify hyperpolarization-activated cation channels modulators for
treating familial sinus rhythm diseases, and ventricular arrhythmias.
XX
PS Claim 13; Page 78; 81pp; English.
XX
CC The present sequence is human hyperpolarisation activated channel 3
(HAC3). This protein comprises an alpha-subunit of a cation channel,
which forms upon hyperpolarisation, a cation channel with an additional
HAC. Modulators of HAC activity are useful for treating various pacemaker
dysfunctions such as familial sinus rhythm diseases, sick sinus syndrome

QY 407 SEPLREEIINFTCKGLVAHMLPAHADPSFTAVLTKLREVPQGDVLVREGSVGRKMY 466
 Db 721 PECLOADIHLNRSLLQHCXKPRGATGCLRALAMKFKTHAPPDGLTVAHGDLLTALY 780
 QY 467 FIOHGLSVLARGARDRLTDSYFGE-ICLLTR-GRRTASVRADTYCRLYSLSVDHFA 524
 Db 781 FISRGSTIELRGDVAAILKNDIFGEPLNLYARPGKNGDVRALTYCDLKHHRDILLE 840
 QY 525 VLEEFPMRRAFAETVAMDRLLRIGKNSILQKRSBPSGSS---GGIMEQH---LV 575
 Db 841 VLDMPFSDHFWMS-SLEITFNLRDNTMI-----PGSPGSTLEGGSQRKRLSFR 893
 QY 576 QHORD-----MARGVGRAPSTGAQLSGKPLVWELVHAPLQAAVTSNVALATH 626
 Db 894 RTDKDTEQGEVAGLGRAGAPSS-----RGRP----- 923
 QY 627 QRGLPLSPDSPATLLARSAMRSAGSPASPLVVRAGPMASTSRLLPAPPARTLHASLSRA 686
 Db 924 -GGPWGESPPSSPESSEDEGPRSSPL---RLVPFSS---PRPP----- 964
 QY 687 GRSQVSLGPPPGS-----GGRRLGPRGRPLSASQPSLPORAT--GDGSPGRKSGSERL 739
 Db 965 -----GPPGGEPLMEDCEKSSDCTNPLSGAFSGVSNIFSWGD-SRGRQYQELPRC 1015
 QY 740 P-PSGLLAKPRTAQP RP 757
 Db 1016 PAPTPLLNLPLSSPGRRP 1034
 RESULT 2
 T31354
 probable potassium channel elk chain 1 - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
 C;Accession: T31354
 R;England, B.; Neu, A.; Ludwig, J.; Roepke, J.; Pong, O.
 submitted to the EMBL Data Library, July 1998
 A;Description: Identification of three rat potassium channel genes homologous to D. melanogaster
 A;Reference number: Z20983
 A;Accession: T31354
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-1017 <ENG>
 A;Cross-references: UNIPROT:Q9R179; UNIPARC:UPI0000170A85; EMBL:AJ007628; NID:e13229997;
 A;Experimental source: cortex
 C;Genetics:
 A;Gene: elk1
 C;Keywords: potassium channel
 Query Match 12.6%; Score 509; DB 2; Length 1017;
 Best Local Similarity 25.3%; Pred. No. 1.7e-24;
 Matches 204; Conservative 118; Mismatches 303; Indels 180; Gaps 29;
 QY 46 RRLHGLTLOFTVKNKSLRVFGSHKA-----VEIEQERVKSGA---AWIHPYSDRRF 94
 Db 170 RQRNRTVLRLTGHGPRDQSGVANSVPEKPSVPEYKVASVGGSCRLHLH-YISPKA 228
 QY 95 YNDLIMLLMVGNLVLPVGIITFFKEENSP-----PMIVFNVLSDTFFLLDLVNLFRGTIV 150
 Db 229 VMDGLILLATFYVAVTVPNVNCVAGDDPTITSRHLTVSDIAVEMVLFILDIILNFTTV 288
 QY 151 VEGEAILLAPAIRTRYRTWFLVDLISIPVD--YIFLVLEPRPLDAEVYKTAARL 208
 Db 289 SOSG-QVWAPRSIGLHYLATWFFVDLIAALPFDLLYVFNIT----- 329
 QY 209 IVRFTKILSLRLRLIRLYHOWEIFHMTYDLASAVRIFNLIGHMMLLCHWDGCL 268
 Db 330 ----VTSVLHLKTVRLRLRLQLKLER-----YSQSAVV-LTLNLSVFAALLAHMCAV 380
 QY 269 QFLV-----PMLQDFPPDCWVSINHMVNSWGRQ-----YSHA 301
 Db 381 WYVIGRREANDPLLDWIG--WL-----HELCKRLEEPYVNSAGSPRSAYIAA 430

QY 302 LEKAMSHMLCIGYGQOAPVGMEDVWLTMLSMIVGATCYAMFIGHATALIQSLDSRRQYO 361
 Db 431 LYFTUSSITSVGFNVNCANTDAEKIFSICTMILGALMAHVFGVNTAIQRYSRSLYH 490
 QY 362 EKYKQVEQYMFHKLPAADTRQRIHEYYEHRYQ-GRMPDEESILGELSPLREIINFCTR 420
 Db 491 SRMKDLKOFIRVHRLPRPLKQRMLEYFQTTWAVNSGIDANELLRDPFDELADIAHMLNR 550
 QY 421 GLVAMPLFAHADPSFTAVLTKLREVPQGDVLVREGSVGRKMYFQHGLLSVLAR-- 478
 Db 551 EIL-QLPLFGAASRGCLRALSLHIXTSFCAPGEFLRRGDALQAHYYVCSSGLEVRDNT 609
 QY 479 -----GARDTRLTDSYFGEICLLTREGRETASVRADTYCRLYSLSVDHFNALVE 527
 Db 610 VLAIGKGDILGADIPELGQBPFGAGCVL---KTSADVKAITYCGLQQLSRSGRLAEVLR 666
 QY 528 EPPMRRRAFETVAMDRL---LRIGKNSILQKRSKP-----SPGSSGGIMEQHLVQ 576
 Db 667 LYPEYVAFRAGLPRDLTFNLRQSENNGLGRFSRPLSQARSOTLSSSDKTLPSITE 726
 QY 577 HDRDMARGVRGRAPSTGAQLSGKPLVWELVHAPLQAAVTSNVAIALTHQRGPIPLSPD 636
 Db 727 TE-----GMEPGAGS---KP-----RRPLLPLNL 748
 QY 637 SPATLLARSAMRSAGSPASPL---VPVRAGPWASTSRLLPAPPARTLHASLSRAGR-SQVS 692
 Db 749 SPA-----RPRGSLVSLIGEELPFPSALVSSPSLSTPT-----SPALAGGSSPS 793
 QY 693 LLGPPPGGGRRRLGPRGRPLSASQPSLPORATGDSPP-----GRKGGSGERLPPSGLLAKP 748
 Db 794 LHGPPRGSA-----WKPQLLTPLTGTFCPPDLSPWIVDIEDSSNTAEAPTRFRSKR 847
 QY 749 PR-TAQP RP RP VPPEPATRGLQLSA 772
 Db 848 PEPTRTSQAPLSGPRLSRELATEA 872
 RESULT 3
 AS5251
 cyclic nucleotide-gated Ca++ channel protein CNG-3 - bovine
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 09-Jul-2004
 C;Accession: AS5251; S43976
 R;Biel, M.; Zong, X.; Distler, M.; Bosse, E.; Klugbauer, N.; Murakami, M.; Flockert, V.
 Proc. Natl. Acad. Sci. U.S.A. 91, 3505-3509, 1994
 A;Title: Another member of the cyclic nucleotide-gated channel family, expressed in tes
 A;Reference number: AS5251; MUID:94224768; PMID:8170936
 A;Accession: AS5251
 A;Status: nucleic acid sequence not shown
 A;Molecule type: mRNA
 A;Residues: 1-706 <BI>
 A;Cross-references: UNIPROT:Q29441; UNIPARC:UPI0000127C20; GB:X76485; NID:g488728; PIDN
 A;Experimental source: kidney
 R;Weinand, I.; Godde, M.; Frings, S.; Weiner, J.; Mueller, F.; Altenhofen, W.; Hatt, H.;
 Nature 368, 859-863, 1994
 A;Title: Cloning and functional expression of a cyclic-nucleotide-gated channel from ma
 A;Reference number: S43976; MUID:94211295; PMID:7512693
 A;Accession: S43976
 A;Status: preliminary; nucleic acid sequence not shown
 A;Molecule type: mRNA
 A;Residues: 1-706 <WE>
 A;Cross-references: UNIPARC:UPI0000127C20; GB:X89600; NID:g908823; PIDN:CAA61759.1; PID
 A;Experimental source: testis
 C;Genetics:
 A;Gene: CNG3
 C;Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide
 C;Keywords: GMP binding; ion channel; ion transport; membrane protein
 F:501-625/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>
 Query Match 12.1%; Score 487.5; DB 2; Length 706;
 Best Local Similarity 26.1%; Pred. No. 2.4e-23;
 Matches 132; Conservative 115; Mismatches 215; Indels 43; Gaps 13;

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model
Run on: June 26, 2006, 20:18:22 ; Search time 46 Seconds
(without alignments)
1618.952 Million cell updates/sec

Title: US-09-767-597-1
Perfect score: 4038
Sequence: 1 MEAEQRPAGASGATPGLE.....PRPVPEPATPRGLQLSANM 774

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80.*
1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	512.5	12.7	1159	2 I38465	probable potassium
2	509	12.6	1017	2 T31354	probable potassium
3	487.5	12.1	706	2 A55251	cyclic nucleotide-
4	485	12.0	695	2 S74179	cyclic nucleotide-
5	483.5	12.0	735	2 I50630	alpha subunit of c
6	483	12.0	664	2 S11517	cyclic nucleotide-
7	478.5	11.8	962	2 I53197	potassium channel
8	473.5	11.7	1174	2 A40853	potassium channel
9	472	11.7	690	1 J07103	CGMP-gated ion cha
10	465.5	11.5	691	2 J06509	rod cyclic nucleot
11	465	11.5	663	2 S11521	CAMP-gated channel
12	463.5	11.5	645	2 I50680	potassium channel
13	462	11.4	732	2 S35691	alpha subunit of r
14	459.5	11.4	682	1 JH0560	cyclic nucleotide-
15	459	11.4	909	2 S32538	CGMP-gated cation
16	454	11.2	688	2 B42161	CGMP-gated cation
17	452	11.2	989	2 I48912	potassium channel
18	449.5	11.1	575	2 I59337	olfactory cyclic n
19	447	11.1	1087	2 T31100	probable potassium
20	445.5	11.0	665	2 S52072	DnMGC protein - f
21	445.5	11.0	686	1 A44842	CGMP-gated ion cha
22	444	11.0	1284	2 T13168	probable potassium
23	438.5	10.9	514	2 T19579	hypothetical prote
24	432.5	10.7	690	2 A42161	CGMP-gated cation
25	409	10.1	1102	2 T17367	potassium channel
26	402.5	10.0	772	2 S28292	hypothetical prote
27	400.5	9.9	934	2 T42394	potassium channel
28	396.5	9.8	828	2 T52046	potassium channel
29	375	9.3	787	2 S68699	potassium channel

30	361	8.9	800	2	T19627	hypothetical prote
31	337	8.3	733	2	E83357	hypothetical prote
32	335	8.3	690	2	G84638	hypothetical prote
33	330.5	8.2	838	2	S23606	potassium channel
34	330.5	8.2	857	2	S62694	potassium channel
35	328	8.1	747	2	T52572	cyclic nucleotide
36	328	8.1	887	2	T03939	potassium channel
37	327.5	8.1	883	2	T07651	potassium channel
38	323.5	8.0	746	2	H86330	probable cyclic nu
39	322	8.0	706	2	F86143	hypothetical prote
40	321.5	8.0	726	2	A85355	hypothetical prote
41	320	7.9	807	2	T12177	potassium channel
42	319.5	7.9	673	2	T20936	hypothetical prote
43	317	7.9	677	2	S32816	potassium channel
44	317	7.9	710	2	T52573	cyclic nucleotide
45	313	7.8	716	2	T51354	cyclic nucleotide-

ALIGNMENTS

RESULT 1

I38465
probable potassium channel subunit - human
C:Species: Homo sapiens (man)
C:Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 09-Jul-2004
C:Accession: I38465
R:Warme, J.W.; Ganetzky, B.
Proc. Natl. Acad. Sci. U.S.A. 91, 3438-3442, 1994
A:Title: A family of potassium channel genes related to eag in Drosophila and mammals.
A:Reference number: A54953; MUID:94211879; PMID:8159766
A:Accession: I38465
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-1159 <RES>
A:Cross-references: UNIPROT:Q12809; UNIPARC:UPI000062255; EMBL:U04270; NID:G487737; PDB:F742-858/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>
Query Match 12.7%; Score 512.5; DB 2; Length 1159;
Best Local Similarity 24.2%; Pred. NO. 1.2e-24;
Matches 208; Conservative 124; Mismatches 322; Indels 205; Gaps 34;

QY	3	AEQPPAGASEGATPGLEAV-PPVAPP-----ATAAGGPIPKSG-----PEPKRHL 49
DB	277	ASVRRASSADD-----IEAMRAGVLPPPPRHASTGAMHPL-RSGLLNSTSDSLVRYRTI 330
QY	50	GTLLQPTVNFKSLRVFG-----SHKAVEIEQERKVSAGA-----83
DB	331	SKIPQITLNFVDLK--GDPFLASPTSDRIIAPKIKERTHNVTI-KVTQVLSLGADVLP 387
QY	84	-----WIHPYSDFRMYWDLIMLLMVGNLIVLPVGITFF---KEENSP-----124
DB	388	YKLOAPRIHRWTLHYSPKAVMDLILLVIYVFTPYSAAFLLKETEEGPPATECGY 447
QY	125	---PWIVFNVLSTPFLDLVNFRCIVVEGAEILLAPRAIRTYRLTWFLVDLISSI 181
DB	448	ACQPLAVDLIVDMFIVDILINFT--TYNNANEEVSHPGRIAVHYFKGFWLIDVMAAI 506
QY	182	PVDYIFLVVELEPRDAEVYKTAARLIRVFTKILSLRLRLSLIRYIHOEEIFHMT 241
DB	507	PFLLIFGSGSEBLIG--LKTRALLRLVRAR-----KLDRISEY-----545
QY	242	YDLASAVRIFNLIENMLLCHWDGCLQFLVPMLOFPDPDQWYSINHMVNHSGROYSH- 300
DB	546	---GAUV--LFLMCTCFALIAHLWACIWAIGNWEQPHMDSRIGLWHLNLDGQIGKPNSS 600
QY	301	-----ALPKAMSHMLCICYGOQAPVGMGPDVWLTMLSMIVGATCYANFTGHAT 347
DB	601	GLGSPSISKQYVATLYFTFSSLTSGVGNVSPNTNSEKIFSIICVMLIGSLMYASIFGNVS 660
QY	348	ALIQSLDSSRRQYQEKYQVQYMSFKLUPADPRQRIHEYYEYHYRQ-QKMFDEESILGEL 406
DB	661	AIIOQLRYSGTARYHTQMLRVREFIRFHQIPNPNURQLEEFYQFQAWSYTNGIDNNAVLKGF 720

CC similarity).

CC -!- SUBUNIT: The potassium channel is probably composed of a homo- or

CC heterotetrameric complex of pore-forming subunits.

CC -!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein.

CC -!- DOMAIN: The segment S4 is probably the voltage-sensor and is

CC characterized by a series of positively charged amino acids at

CC every third position.

CC -!- SIMILARITY: Belongs to the potassium channel family. HCN

CC subfamily.

CC -!- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.

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CC -----

CC EMBL; AL713999; CAI95100.1; -; Genomic_DNA.

CC DR EMBL; AB040968; BA96059.2; -; mRNA.

CC DR EMBL; BC000066; AAH00066.1; -; mRNA.

CC DR EMBL; BC028024; AAH28024.2; ALT_INIT; mRNA.

CC DR SMR; Q9P123; 354-554.

CC DR Ensembl; ENSG00000143630; Homo sapiens.

CC DR HGNC; HGNC:19183; HCN3.

CC DR InterPro; IPR000595; CNMP bd.

CC DR InterPro; IPR003938; EAG_ELK_ERG.

CC DR InterPro; IPR005821; Ion trans.

CC DR InterPro; IPR005820; M+channel_nlg.

CC DR Pfam; PF00027; CNMP_binding; 1.

CC DR Pfam; PF00520; Ion trans; 1.

CC DR PRINTS; PR01463; EAGCHANLMFLY.

CC DR SMART; SM00100; CNMP; 1.

CC DR PROSITE; PS00888; CNMP_BINDING_1; FALSE_NEG.

CC DR PROSITE; PS00889; CNMP_BINDING_2; FALSE_NEG.

CC DR PROSITE; PS0042; CNMP_BINDING_3; 1.

CC DR CAMP; CAMP-binding; Glycoprotein; Ion transport; Ionic channel;

CC Membrane; Nucleotide-binding; Potassium; Potassium channel;

CC Potassium transport; Sodium; Sodium channel; Sodium transport;

CC Transmembrane; Transport; Voltage-gated channel;

CC CHAIN 1 774

CC activated cyclic nucleotide-gated channel

CC 3

CC /FTID=PRO 0000054114.

CC TOPO_DOM 1 97

CC TRANSMEM 98 118

CC TRANSMEM 125 145

CC TOPO_DOM 146 171

CC TRANSMEM 172 192

CC TRANSMEM 202 222

CC TOPO_DOM 223 253

CC TRANSMEM 254 274

CC TRANSMEM 298 319

CC TRANSMEM 330 350

CC TOPO_DOM 351 774

CC NP_BIND 428 545

CC REGION 46 91

CC COMPBIAS 696 765

CC CARBOHYD 291 291

CC CONFLICT 206 206

CC CONFLICT 734 734

CC SEQUENCE 774 AA; 86032 MW; 37B9BC13E5E2C097 CRC64;

Query Match 100.0%; Score 4038; DB 1; Length 774;

Best Local Similarity 100.0%; Pred. No. 4.7e-226;

Matches 774; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEAEORPAAGSEGTATGTAAGVPPVAPPAAGSGPIPKSGPEPKRRHLGTLLOFTVNF 60

DB 1 MEAEORPAAGSEGTATGTAAGVPPVAPPAAGSGPIPKSGPEPKRRHLGTLLOFTVNF 60

QY 61 SLRVFGSHKAVEIEQERVKAGAWIHPYSDPRFYWDIMLLMGNLIVLPVGTTPPE 120

DB 61 SLRVFGSHKAVEIEQERVKAGAWIHPYSDPRFYWDIMLLMGNLIVLPVGTTPPE 120

QY 121 ENSPPWIVFNVLSDTFFLLDLVFNFRGTGVVEEAGAILLAPRAIRTRYLRTWFLVDLISS 180

DB 121 ENSPPWIVFNVLSDTFFLLDLVFNFRGTGVVEEAGAILLAPRAIRTRYLRTWFLVDLISS 180

QY 181 IPVDYIFLWVELEPRDLAEVYKTARALRIVRFTKILSLRLRLSLRILRYIHQWEEIAPHM 240

DB 181 IPVDYIFLWVELEPRDLAEVYKTARALRIVRFTKILSLRLRLSLRILRYIHQWEEIAPHM 240

QY 241 TYDLASAVRIFNLIGWMLLCHWDGCLQFLVPMQLQDFPPDCWVSINHMHNSGRQYSH 300

DB 241 TYDLASAVRIFNLIGWMLLCHWDGCLQFLVPMQLQDFPPDCWVSINHMHNSGRQYSH 300

QY 301 ALFKAMSHMLCIGYGOQAPVGMPPDWLTMLSMIVGATCYAMFIGHATALIQSLDSSRRQY 360

DB 301 ALFKAMSHMLCIGYGOQAPVGMPPDWLTMLSMIVGATCYAMFIGHATALIQSLDSSRRQY 360

QY 361 QEKYQVEQYNSPHKLPAIDTRQRIHEYEHRYQKMFDEESILGELSEPLREEINFTCR 420

DB 361 QEKYQVEQYNSPHKLPAIDTRQRIHEYEHRYQKMFDEESILGELSEPLREEINFTCR 420

QY 421 GLVAHMLPLFAHADPSFVTAIVLTKLRFVFOGDLVREGSVGRKMYFIQHGLLSVLARGA 480

DB 421 GLVAHMLPLFAHADPSFVTAIVLTKLRFVFOGDLVREGSVGRKMYFIQHGLLSVLARGA 480

QY 481 RDTLTDGYSYFGEICLLTRGRRTASVRADTYCRILSYSLVDHFNALVEEFPMMRRAFETVA 540

DB 481 RDTLTDGYSYFGEICLLTRGRRTASVRADTYCRILSYSLVDHFNALVEEFPMMRRAFETVA 540

QY 541 MDRLRLRGKNSILQKRSEPSPGSSGIMEQHLVQHDRDMARGVGRAPSTGALSCKP 600

DB 541 MDRLRLRGKNSILQKRSEPSPGSSGIMEQHLVQHDRDMARGVGRAPSTGALSCKP 600

QY 601 VLWEPLVHAPLQAAVTSNVAIALTHORGLPLSPDSPATLLARSASRSGSPASPLVPV 660

DB 601 VLWEPLVHAPLQAAVTSNVAIALTHORGLPLSPDSPATLLARSASRSGSPASPLVPV 660

QY 661 RAGWASTSLRPLAPPARTLHASLRAGRSQVSLGGPPGGGRLGPRGRPLSASQPSLP 720

DB 661 RAGWASTSLRPLAPPARTLHASLRAGRSQVSLGGPPGGGRLGPRGRPLSASQPSLP 720

QY 721 QRATGDSGPKSGSGSERLPPSGLLAKPRTAQPRTVPPEPATPRGLQLSANM 774

DB 721 QRATGDSGPKSGSGSERLPPSGLLAKPRTAQPRTVPPEPATPRGLQLSANM 774

RESULT 2

ID Q86WJ5 HUMAN PRELIMINARY; PRT; 774 AA.

AC Q86WJ5;

DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.

DT 01-JUN-2003, sequence version 1.

DT 07-FEB-2006, entry version 11.

DE Hyperpolarization activated cyclic nucleotide-gated potassium channel.

GN Name=HCN3;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Homo.

OX NCBI_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Brain;

RA Liu Y., Folander K., Swanson R.;

EL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.

CC -----

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CC -----

CC EMBL; AF488550; AA049470.1; -; mRNA.

CC DR HSP; O88703; I03E

CC SMR; Q86WJ5; 354-554.

CC Ensembl; ENSG00000143630; Homo sapiens.

CC DR GO; GO:0016020; C:membrane; IEA.

CC DR GO; GO:0005261; F:cation channel activity; IEA.

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Kryzhanvskii M.I., Skalska U.E., Schnurch A., Schein J.E., Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

273 PMLQDFPDCWVSINNMVNSWGRQSHALFKAMSHMLCIGYGOQAPVGMDSVWLTMLSM 332
 346 PMLQDFPDCWVSINNMVNSWGRQSHALFKAMSHMLCIGYGOQAPVGMDSVWLTMLSM 405
 333 IVGATCYAMFIGHATALIQLSDSSRRQYQEKYQVEQYMSFHKLPADTRQRIHEYYEHRY 392
 406 IVGATCYAMFIGHATALIQLSDSSRRQYQEKYQVEQYMSFHKLPADTRQRIHEYYEHRY 465
 393 QGKMFDEESILGELSEPLEREEIINFCTCRGLVAHMLPLFAHADPSFVTVAVLTKLRFVFPQ 452
 466 QGKMFDEESILGELSEPLEREEIINFCTCRGLVAHMLPLFAHADPSFVTVAVLTKLRFVFPQ 525
 453 DLVREGSVGRKMYFIQHLGLSVLARGARDTRTDGSGYFGEICLLTRGRTTASVRADTYC 512
 526 DVIIREGTIGKMYFIQHLGLSVLARGARDTRTDGSGYFGEICLLTRGRTTASVRADTYC 585
 513 RLYSLSDVHNFNAVLEBPPMRRAPFETVMDRLRIGKNSILQKRSSEPPSGSGGIME- 571
 586 RLYSLSDVHNFNAVLEBPPMRRAPFETVMDRLRIGKNSILQKRSSEPPSGSGGIME- 645
 572 ---OHLVQHDREMAHCAHVRQAASATPTPTVWITPLIQAPLQAAAATTSVAIALTH- 628
 646 EIIQOIVQHDREMAHCAHVRQAASATPTPTVWITPLIQAPLQAAAATTSVAIALTH- 704
 629 GPLPLSPDSPATLL---ARSASWRSAGSPASP-----LVPVRAG---PWASTSRPLPAP 674
 705 -----PRLPAAIFRPPPGSGLNLGAGQTPRHLKRLQSLIPSLGASPASSPSQVDT 758
 675 PARTLH-----ASLSR-AGRSQV---SLLGPPPPGGG-----R 703
 759 SSSSFHIQQLAGFAPAGLSPLLPSSSSPPPGACGSPSAPTSPAGVAATTIAGFGPHK 818
 704 RLQ-----PRGRPLSASOPS-LPQRATG-----DGSP 729
 819 ALGGLSSSDSPLLTLPQPGARSQAQSPAPPGARGGLGLPEHFLPPPPSSRSPSSP 878
 730 GRKGSGERLPPS-----GLLAKPPRTAQ-PPRPVP-----EPA--TPRG 767
 879 GOLQO-----PPGELSLGLATGPLSTPTPTPPRQPEPPLVAGASGASPVGFTPRG 929

RESULT 2

US-949-016-6615
 ; Sequence 6615, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 6615
 ; LENGTH: 1203
 ; TYPE: PRI
 ; ORGANISM: Human
 ; US-09-949-016-6615

Query Match 62.9%; Score 2540; DB 2; Length 1203;
 Best Local Similarity 59.6%; Pred. No. 2.7e-217;
 Matches 534; Conservative 72; Mismatches 144; Indels 146; Gaps 19;
 4 EORPAAGASGATPGLEAVPPVAPPATTAASGPIKSGPEPK-----45
 142 DRTFPGLEAEPERPGASQAAPASPPPPPPQPPQPPASASCEQPSVDTAIVKVEGGAAGDQIL 201

46 -----RHLGLTLOPTVNKESLAVFGSHKAVEIEORVKKSAGAWIHPYSDF 92
 202 PEAEVRLGOAGFMQKQFAGMLQPGVKNKFLRMFSGQKAVEIEORVKKSAGAWIHPYSDF 261
 93 RPYMDLIMLLMVGNLIVLPVGIITPFKEENSPPMIVFNVLSDTFFFLDLVNLFRGTGIVVE 152
 262 RPYMDLIMLLMVGNLIIIPVGIITPFKEENSPPMIVFNVLSDTFFFLDLVNLFRGTGIVVE 321
 153 EGAEILLAPRAIRTRYLTWFLVDLISSIPVDYIPLVVELEPRDLDAEYTKARALRIVRF 212
 322 DNTIELDQRIKMKYKSWFMDVFISSIPVDYIPLV--ETRIDSEYTKARALRIVRF 379
 213 TKILSLRLRLRLRIYIHOWEEIFHMTYDILASAVRIFNLIGMMLLCHWDGCLQFLV 272
 380 TKILSLRLRLRLRIYIHOWEEIFHMTYDILASAVRIFNLIGMMLLCHWDGCLQFLV 439
 273 PMLQDFPDCWVSINNMVNSWGRQSHALFKAMSHMLCIGYGOQAPVGMDSVWLTMLSM 332
 440 PMLQDFPDCWVSINNMVNSWGRQSHALFKAMSHMLCIGYGOQAPVGMDSVWLTMLSM 499
 333 IVGATCYAMFIGHATALIQLSDSSRRQYQEKYQVEQYMSFHKLPADTRQRIHEYYEHRY 392
 500 IVGATCYAMFIGHATALIQLSDSSRRQYQEKYQVEQYMSFHKLPADTRQRIHEYYEHRY 559
 393 QGKMFDEESILGELSEPLEREEIINFCTCRGLVAHMLPLFAHADPSFVTVAVLTKLRFVFPQ 452
 560 QGKMFDEESILGELSEPLEREEIINFCTCRGLVAHMLPLFAHADPSFVTVAVLTKLRFVFPQ 619
 453 DLVREGSVGRKMYFIQHLGLSVLARGARDTRTDGSGYFGEICLLTRGRTTASVRADTYC 512
 620 DVIIREGTIGKMYFIQHLGLSVLARGARDTRTDGSGYFGEICLLTRGRTTASVRADTYC 679
 513 RLYSLSDVHNFNAVLEBPPMRRAPFETVMDRLRIGKNSILQKRSSEPPSGSGGIME- 571
 680 RLYSLSDVHNFNAVLEBPPMRRAPFETVMDRLRIGKNSILQKRSSEPPSGSGGIME- 739
 572 ---OHLVQHDREMAHCAHVRQAASATPTPTVWITPLIQAPLQAAAATTSVAIALTH- 798
 740 EIIQOIVQHDREMAHCAHVRQAASATPTPTVWITPLIQAPLQAAAATTSVAIALTH- 798
 629 GPLPLSPDSPATLL---ARSASWRSAGSPASP-----LVPVRAG---PWASTSRPLPAP 674
 799 -----PRLPAAIFRPPPGSGLNLGAGQTPRHLKRLQSLIPSLGASPASSPSQVDT 852
 675 PARTLH-----ASLSR-AGRSQV---SLLGPPPPGGG-----R 703
 853 SSSSFHIQQLAGFAPAGLSPLLPSSSSPPPGACGSPSAPTSPAGVAATTIAGFGPHK 912
 704 RLQ-----PRGRPLSASOPS-LPQRATG-----DGSP 729
 913 ALGGLSSSDSPLLTLPQPGARSQAQSPAPPGARGGLGLPEHFLPPPPSSRSPSSP 972
 730 GRKGSGERLPPS-----GLLAKPPRTAQ-PPRPVP-----EPA--TPRG 767
 973 GOLQO-----PPGELSLGLATGPLSTPTPTPPRQPEPPLVAGASGASPVGFTPRG 1023

RESULT 3

US-10-067-457-3
 ; Sequence 3, Application US/10067457
 ; Patent No. 6979532
 ; GENERAL INFORMATION:
 ; APPLICANT: Aventis Pharma Deutschland GmbH
 ; TITLE OF INVENTION: Process for identifying substances which modulate the
 ; activity of hyperpolarization-activated cation channels
 ; FILE REFERENCE: AVE D-2000/A006
 ; CURRENT APPLICATION NUMBER: US/10/067,457
 ; CURRENT FILING DATE: 2002-04-09
 ; PRIOR APPLICATION NUMBER: US/09/779,587
 ; PRIOR FILING DATE: 2001-02-09
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: PatentIn Ver. 2.1

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 26, 2006, 20:22:41 ; Search time 53 Seconds
(without alignments)
1278.277 Million cell updates/sec

Title: US-09-767-597-1

Perfect score: 4038

Sequence: 1 MEAEQRPAGASGATGPLE.....PRPVPPEPATRGQLQSANM 774

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum-Match 100%

Logging flyst 45 summaries

Database :

- Issued patents AA.*
- 1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5 COMB.pcp.*
 - 2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6 COMB.pcp.*
 - 3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7 COMB.pcp.*
 - 4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H COMB.pcp.*
 - 5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS COMB.pcp.*
 - 6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE COMB.pcp.*
 - 7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfilese1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2540	62.9	1109	2	US-09-949-016-10771
2	2540	62.9	1203	2	US-09-949-016-6615
3	2540	62.9	1203	2	US-10-067-457-3
4	2402	59.5	855	2	US-09-949-016-7263
5	2402	59.5	889	2	US-09-949-016-6036
6	2402	59.5	889	2	US-10-067-457-1
7	2391.5	59.2	863	2	US-10-067-457-5
8	2316	57.4	910	2	US-08-997-685A-2
9	2316	57.4	910	2	US-09-086-436-31
10	2251	55.7	597	2	US-09-086-436-41
11	2248	55.7	597	2	US-08-997-685A-12
12	2216	54.9	749	2	US-08-997-685A-10
13	2216	54.9	749	2	US-09-086-436-39
14	2202.5	54.5	504	2	US-09-086-436-33
15	2199.5	54.5	528	2	US-08-997-685A-4
16	2154	53.3	506	2	US-08-997-685A-6
17	2143	53.1	506	2	US-09-086-436-35
18	858.5	21.3	308	2	US-09-270-767-32667
19	858.5	21.3	308	2	US-09-270-767-47884
20	524	13.0	1017	2	US-09-600-776-6
21	524	13.0	1017	2	US-09-965-830-6
22	512.5	12.7	905	2	US-10-104-047-2728
23	512.5	12.7	1159	1	US-08-956-242-13
24	512.5	12.7	1159	2	US-09-351-215-13
25	512.5	12.7	1159	2	US-09-226-012-2
26	512.5	12.7	1159	2	US-09-226-012-4

27	512.5	12.7	1159	2	US-09-358-383C-10	Sequence 10, Appl
28	512.5	12.7	1159	2	US-09-375-252A-12	Sequence 12, Appl
29	509	12.6	131	2	US-08-997-685A-45	Sequence 45, Appl
30	505	12.5	119	2	US-08-997-685A-53	Sequence 53, Appl
31	493.5	12.2	694	2	US-09-538-092-1351	Sequence 1351, Ap
32	493.5	12.2	698	2	US-09-949-016-10215	Sequence 3, Appl
33	486.5	12.0	962	2	US-09-694-777A-3	Sequence 9, Appl
34	485	12.0	962	2	US-09-614-480-9	Sequence 9, Appl
35	485	12.0	962	2	US-10-422-075-9	Sequence 21, Appl
36	481.5	11.9	960	2	US-09-694-777A-21	Sequence 4, Appl
37	477	11.8	989	2	US-09-694-777A-24	Sequence 24, Appl
38	476.5	11.8	962	2	US-09-614-480-2	Sequence 2, Appl
39	475.5	11.8	988	2	US-10-162-012-5	Sequence 5, Appl
40	475.5	11.8	988	2	US-10-422-075-2	Sequence 2, Appl
41	475.5	11.7	988	2	US-10-162-012-12	Sequence 12, Appl
42	474	11.7	988	2	US-09-694-777A-22	Sequence 22, Appl
43	472	11.7	987	2	US-09-538-092-1315	Sequence 1315, Ap
44	466	11.5	909	2	US-09-927-267-1	Sequence 1, Appl
45	456.5	11.3	575	2	US-09-927-267-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1

US-09-949-016-10771
; Sequence 10771, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10771
; LENGTH: 1109
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-10771

Query Match 62.9%; Score 2540; DB 2; Length 1109;
Best Local Similarity 59.8%; Pred. No. 2.4e-217;
Matches 534; Conservative 72; Mismatches 144; Indels 146; Gaps 19;

QY	4	EQRPAGASGATGPLEAVPPVAPPATAGSGPIKSGPEPK-----	45
DB	48	DRTPGLAAEPERPGASQAPASPPPPQPPQPPASASCEQPSVDTAIKVEGGAAGDQIL	107
QY	46	-----RRHLGTLLOFTVNFKSLRVFGSHKAVEIQEVRKVSAGAWIHPYSDF	92
DB	108	PEAEVRLGQAGFMQRQGMALQGVNKFSLRMFGSQKAVEQERVKVSAGWIHPYSDF	167
QY	93	RFVWDLMLLMVGNLIVLPVGTTFPKENSPPWIVNFVLSDTFFLLDLVNFRTGIWE	152
DB	168	RFVWDLTMLLMVGNLIIIPVGTTFPKDENTTTPWIVNFVNSDTFFLLDLVNFRTGIWE	227
QY	153	EGAEILLAPRAIRTYRLTWFLVDLSSIPVDYIFLVVELEPRLDAAVYKTARALRVRF	212
DB	228	DNTEILLDPQRIKKTKLKSFWFDFISSIPVDYIFLV--ETRIDSEVYKTARALRVRF	285
QY	213	TKILSLRLRLRLRLRYHQWEEIFHMTYDLSAVVRIFNLIGMMLLLCHWDGCLQFLV	272
DB	286	TKILSLRLRLRLRLRYHQWEEIFHMTYDLSAVVRIVNLIGMMLLLCHWDGCLQFLV	345

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.
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Run on: June 26, 2006, 20:39:12 ; Search time 182 Seconds
(without alignments)
1969.936 Million cell updates/sec
Title: US-09-767-597-1
Perfect score: 4038
Sequence: 1 MEAEQPPAAGASEGATPGLE.....PRPPVPEPATRGLQLSANM 774
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 2097797 seqs, 463214858 residues
Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : Published Applications AA Main:
1: /EMC_Celerra_SIDS3/prodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /EMC_Celerra_SIDS3/prodata/2/pubpaa/US08_PUBCOMB.pep.*
3: /EMC_Celerra_SIDS3/prodata/2/pubpaa/US09_PUBCOMB.pep.*
4: /EMC_Celerra_SIDS3/prodata/2/pubpaa/US10_PUBCOMB.pep.*
5: /EMC_Celerra_SIDS3/prodata/2/pubpaa/US10B_PUBCOMB.pep.*
6: /EMC_Celerra_SIDS3/prodata/2/pubpaa/US11_PUBCOMB.pep.*
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES					%		Query Match		Length DB ID		Description	
Result No.	Score	Score	Length	DB ID								
1	4038	100.0	774	3	US-09-548-933-1		Sequence 1, Appli		Sequence 1, Appli		Sequence 1, Appli	
2	4038	100.0	774	4	US-10-158-684-10		Sequence 10, Appl		Sequence 10, Appl		Sequence 10, Appl	
3	4038	100.0	774	4	US-10-158-711-10		Sequence 10, Appl		Sequence 10, Appl		Sequence 10, Appl	
4	4038	100.0	774	4	US-10-332-447-25		Sequence 25, Appl		Sequence 25, Appl		Sequence 25, Appl	
5	3670	90.9	703	4	US-10-311-795-8		Sequence 8, Appli		Sequence 8, Appli		Sequence 8, Appli	
6	2540	62.9	1203	4	US-10-067-457-3		Sequence 3, Appli		Sequence 3, Appli		Sequence 3, Appli	
7	2540	62.9	1203	4	US-10-311-795-6		Sequence 6, Appli		Sequence 6, Appli		Sequence 6, Appli	
8	2540	62.9	1245	4	US-10-276-774-2323		Sequence 2323, Ap		Sequence 2323, Ap		Sequence 2323, Ap	
9	2402	59.5	889	4	US-10-067-457-1		Sequence 1, Appli		Sequence 1, Appli		Sequence 1, Appli	
10	2402	59.5	889	4	US-10-311-795-4		Sequence 4, Appli		Sequence 4, Appli		Sequence 4, Appli	
11	2402	59.5	889	5	US-10-756-149-5170		Sequence 5170, Ap		Sequence 5170, Ap		Sequence 5170, Ap	
12	2391.5	59.2	863	4	US-10-067-457-5		Sequence 5, Appli		Sequence 5, Appli		Sequence 5, Appli	
13	2391	59.2	875	3	US-09-548-933-15		Sequence 15, Appl		Sequence 15, Appl		Sequence 15, Appl	
14	2350	58.2	882	5	US-10-343-903-11		Sequence 11, Appl		Sequence 11, Appl		Sequence 11, Appl	
15	2346	58.1	882	4	US-10-768-158-38		Sequence 38, Appl		Sequence 38, Appl		Sequence 38, Appl	
16	2346	58.1	890	4	US-10-158-684-4		Sequence 4, Appli		Sequence 4, Appli		Sequence 4, Appli	
17	2346	58.1	890	4	US-10-158-711-4		Sequence 4, Appli		Sequence 4, Appli		Sequence 4, Appli	
18	2346	58.1	890	4	US-10-296-270-4		Sequence 4, Appli		Sequence 4, Appli		Sequence 4, Appli	
19	2346	58.1	890	4	US-10-287-226-352		Sequence 352, App		Sequence 352, App		Sequence 352, App	
20	2345	58.1	837	5	US-10-466-992-20		Sequence 20, Appl		Sequence 20, Appl		Sequence 20, Appl	
21	2344	58.0	890	5	US-10-466-992-16		Sequence 16, Appl		Sequence 16, Appl		Sequence 16, Appl	
22	2341	58.0	890	4	US-10-296-270-8		Sequence 8, Appli		Sequence 8, Appli		Sequence 8, Appli	
23	2341	58.0	890	5	US-10-466-992-10		Sequence 10, Appl		Sequence 10, Appl		Sequence 10, Appl	
24	2340	57.9	890	5	US-10-466-992-2		Sequence 2, Appli		Sequence 2, Appli		Sequence 2, Appli	
25	2340	57.9	890	5	US-10-466-992-14		Sequence 14, Appl		Sequence 14, Appl		Sequence 14, Appl	
26	2340	57.9	890	5	US-10-466-992-18		Sequence 18, Appl		Sequence 18, Appl		Sequence 18, Appl	
27	2340	57.9	890	5	US-10-466-992-19		Sequence 19, Appl		Sequence 19, Appl		Sequence 19, Appl	

28	2333	57.8	890	5	US-10-466-992-8		Sequence 8, Appli		Sequence 8, Appli		Sequence 8, Appli	
29	2333	57.8	890	5	US-10-466-992-12		Sequence 12, Appl		Sequence 12, Appl		Sequence 12, Appl	
30	2332	57.8	890	5	US-10-466-992-4		Sequence 4, Appli		Sequence 4, Appli		Sequence 4, Appli	
31	2329	57.7	890	5	US-10-466-992-6		Sequence 6, Appli		Sequence 6, Appli		Sequence 6, Appli	
32	2325.5	57.6	827	4	US-10-296-270-2		Sequence 2, Appli		Sequence 2, Appli		Sequence 2, Appli	
33	2321.5	57.5	827	4	US-10-296-270-6		Sequence 6, Appli		Sequence 6, Appli		Sequence 6, Appli	
34	2317	57.4	910	5	US-10-466-992-21		Sequence 21, Appl		Sequence 21, Appl		Sequence 21, Appl	
35	2316	57.4	910	3	US-09-086-436-31		Sequence 31, Appl		Sequence 31, Appl		Sequence 31, Appl	
36	2316	57.4	910	4	US-10-753-991-31		Sequence 31, Appl		Sequence 31, Appl		Sequence 31, Appl	
37	2316	57.4	910	5	US-10-384-107-2		Sequence 2, Appli		Sequence 2, Appli		Sequence 2, Appli	
38	2316	57.4	910	5	US-10-466-992-22		Sequence 22, Appl		Sequence 22, Appl		Sequence 22, Appl	
39	2314	57.3	890	4	US-10-311-795-2		Sequence 2, Appli		Sequence 2, Appli		Sequence 2, Appli	
40	2298	56.9	898	5	US-10-466-992-23		Sequence 23, Appl		Sequence 23, Appl		Sequence 23, Appl	
41	2251	55.7	597	3	US-09-086-436-41		Sequence 41, Appl		Sequence 41, Appl		Sequence 41, Appl	
42	2251	55.7	597	4	US-10-753-991-41		Sequence 41, Appl		Sequence 41, Appl		Sequence 41, Appl	
43	2248	55.7	597	5	US-10-384-107-12		Sequence 12, Appl		Sequence 12, Appl		Sequence 12, Appl	
44	2216	54.9	749	3	US-09-086-436-39		Sequence 39, Appl		Sequence 39, Appl		Sequence 39, Appl	
45	2216	54.9	749	4	US-10-753-991-39		Sequence 39, Appl		Sequence 39, Appl		Sequence 39, Appl	

ALIGNMENTS

RESULT 1
US-09-548-933-1
; Sequence 1, Application US/09548933
; Publication No. US20030044889A1
; GENERAL INFORMATION:
; APPLICANT: Jega, Timothy James
; APPLICANT: ICGen, Inc.
; TITLE OF INVENTION: Human HOC3
; FILE REFERENCE: 018512-002210US
; CURRENT APPLICATION NUMBER: US/09/548,933
; CURRENT FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: US 60/129,456
; PRIOR FILING DATE: 1999-04-15
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 774
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human hyperpolarization-activated voltage-gated
; OTHER INFORMATION: cation channel 3 (HAC3)
US-09-548-933-1

Query Match		100.0%	Score 4038;	DB 3;	Length 774;
Best Local Similarity		100.0%	Pred. No. 1.1e-282;		
Matches 774;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MEAEQPPAAGASEGATPGLEAVPPVAPPATTAASGPIPKSGPEPKRHGLTLLQPTVNF	60		
Db	1	MEAEQPPAAGASEGATPGLEAVPPVAPPATTAASGPIPKSGPEPKRHGLTLLQPTVNF	60		
Qy	61	SLRVFQSHKAVTEQSRVKSAGAWIHPYSDRFFYWDLMILLMVGNIIVLPVGIITFFKE	120		
Db	61	SLRVFQSHKAVTEQSRVKSAGAWIHPYSDRFFYWDLMILLMVGNIIVLPVGIITFFKE	120		
Qy	121	ENSPPMIVFNVLSDTFFLLDLVLPFTGTWSEGAIIAPRAIRYLRITWFLVDLISS	180		
Db	121	ENSPPMIVFNVLSDTFFLLDLVLPFTGTWSEGAIIAPRAIRYLRITWFLVDLISS	180		
Qy	181	IPVDYIFLVELEPRDAEYKTAARALIRVFRFKILSLRLRLSLRLIRYIHOWEIEIFHM	240		
Db	181	IPVDYIFLVELEPRDAEYKTAARALIRVFRFKILSLRLRLSLRLIRYIHOWEIEIFHM	240		
Qy	241	TYDLASAVRIFNLMIGNMLLCHWDCLQFLVPMLODFPDCWVSINHMVNSWGQYSH	300		
Db	241	TYDLASAVRIFNLMIGNMLLCHWDCLQFLVPMLODFPDCWVSINHMVNSWGQYSH	300		
Qy	301	ALFKASHMLCIGYGGOAPVGMDDVWLTMLSMTVGATCYAMFIGHATALIQSLDSSROY	360		

149 EEEKTKKDAIVDPSSNLYRRLTAIALPVFNWLLICRACFDLQSEYLMWLVLDY 208
132 LSTFFLLDLNFRGTGIVVEGAEILLAPRAIRTRYLRTWFLVDLISSIPVDYIFLVE 191
209 SADVLVLDVLRVARTGF-LEQGLMVSDTNRLMQHYKTTTQFKLDVLSVPTDLAYL--- 264
192 LEPRDLAEVYKTARALIRVRFKILSLRLRLSLRIRYIHOWEEIFHMTYDLASAVVRI 251
265 -----KVGNTNPEVRFN-----RLKFSRLFFEDRT-----TRTNYPNMFRI 303
252 FNLIGHMMLLCHWDGCLQFLVPMLODPPDCWVSINHMV--NHSWGRQYSHALFKAMSHM 309
304 GNLVLVLIILHWNACIYPAISKFIGFGTDSWYVNPISPEHGRSLRKIYSLYNSTLTL 363
310 LCIGYGOQAPVGMDFWLTWLSMIVGATCYAMPIGHATALIOSLDSRRQYOEKVKQVEQ 369
364 TTIG-ETPPPVKDEEYLFVVVDPLVGLIFATVGNVGMISNMNASRAEFOAKIDSIRQ 422
370 YMSFHLKLPADTRORIEHYEYHRQY-KMPDEESILGELSEPLREEEINFTCRGLVAHMLP 428
423 YMQFRKVTQDLETRVTRWFDYLMWANKTVDKEVLSKSLDKUAEIAINHLDTLKKVRI 482
429 FAHADPSFTAVTLKLFVFOQGLVVRGSGVGRWYFIQHGLLSVLARG--ARDTRLT 486
483 FQDCEAGLLVELVLRPTVFSFGDYICKGDIGKEMWIIINEGKLAVADDGVTQPVVLS 542
487 DGSYFGEICLL-----TGRRRTASVRADTYCHLSYSLVDHFNVALEPFPMMRRAPETVA 540
543 DGSYFGEISILNTKSGKSGNRRTANIRSGYDLFCLSKDDLMEALTEYPEAKALEEG 602
541 MDLRLAIGKKNSTLQKRSEP 561
603 RQILMKONLIDELARAGADP 623

RESULT 2
US-11-312-958-30
Sequence 30, Application US/11312958
Publication No. US20060100152A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Silos-Santiago, Immaculada
TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING
TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 9949, 14230, 760, 62553,
TITLE OF INVENTION: 12216, 17719, 41897, 47174, 33408, 10002, 16209, 314, 636,
TITLE OF INVENTION: 27410, 33260, 619, 15985, 69112, 2158, 224, 615, 44373,
TITLE OF INVENTION: 95431, 22245, 2387, 16658, 55054, 16314, 1613, 1675, 9569 OR
TITLE OF INVENTION: 13424 MOLECULES
FILE REFERENCE: MPI02-027PIRNMNIM
CURRENT APPLICATION NUMBER: US/11/312,958
CURRENT FILING DATE: 2005-12-20
PRIOR APPLICATION NUMBER: US/10/369,022
PRIOR FILING DATE: 2003-02-19
PRIOR APPLICATION NUMBER: US 60/360,495
PRIOR FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 60/370,121
PRIOR FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: US 60/373,010
PRIOR FILING DATE: 2002-04-16
PRIOR APPLICATION NUMBER: US 60/373,908
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: US 60/377,717
PRIOR FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: US 60/379,949
PRIOR FILING DATE: 2002-05-13
PRIOR APPLICATION NUMBER: US 60/382,409
PRIOR FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: US 60/385,280
PRIOR FILING DATE: 2002-06-03
PRIOR APPLICATION NUMBER: US 60/386,879
PRIOR FILING DATE: 2002-06-06

Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 64
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 30
LENGTH: 989
TYPE: PRT
ORGANISM: Homo sapiens
US-11-312-958-30

Query Match 11.8%; Score 477; DB 7; Length 989;
Best Local Similarity 23.0%; Pred. No. 1.6e-25;
Matches 192; Conservative 129; Mismatches 338; Indels 174; Gaps 27;

QY 31 TAASGPFPKSGPE-----PKRRHLGTLLOPTVKNFSLRVFGSHKAVEIQEERKVSAGA 83
Db 159 TSSRGVIOQLAPSVQKGENVHCHSLAEVLO-----LGSIDLPOYKQEAQKTPPH 208
QY 84 WIIHPYSDRFYFWDILMILLMGNLIVLPVGTITFFKEENSPPIVFNVLSDTFFLLDLVL 143
Db 209 IILH-YCVFKTTDWIILITFTAILVPYVNSFKTRONNVAVLVDSDIVDIPLVDIVL 267
QY 144 NFRGIVVEGAEILLAPRAIRTRYLRTWFLVDLISSIPVDYI-----FL----- 188
Db 268 NFHTTFVGPAG-EVISDPKLIRMYLKTWFVIDLSCLPYDVINAFENVVDSVAFMGDPG 326
QY 189 ----VVELEPRDLAEVYKTARALIRVRFKILSLRLRLSLRIRYIHOWEEIFHMTYDL 244
Db 327 KIGFADQIPPPLEGRESOGISSL-----FSS-LKVVRLRLRGVARKLDHYIE-----YGA 376
QY 245 ASAVVRIENLIGMMLLCHWDGCLQFLVPMLODPPDCWVSINHMVNSWGRQ----- 297
Db 377 AVLVL-----LVCVFLAAHWMACIWSIGDYEIDED-----TKIRNNSWLQLAWDIGT 428
QY 298 -----YSHALFKAMSHMLCIGYGOQAPVGMDFWLTWLSMIVGA 336
Db 429 PYQFNGSGSGKEGPGSKNSYISSLFTMTSLTSVGFNTAPSTDIEKIFAVAIMMIGS 488
QY 337 TCYAMFIGHTALIQSLDSRRQYOEKVKQVEYMSFHLKPADTRORIEHYEYHRQY-OGK 395
Db 489 LLYATIFGNVTTFQOMYANTNRHEMLNSVRDFELKYQVPGKLSERVMDIVSTWSMR 548
QY 396 MFDEESILGELSEPLREEEINFTCRGLVAHMLPFAHADPSFTAVTLKLFVFOQGLV 455
Db 549 GIDTEKVLQICPKDMRADICVHLNRKVFEHPAFRLASDGCCLRALAMEFQTVHCAPGDLI 608
QY 456 VREGSVGRKMYFIQHGLLSVLARGARDTRLTDGSGYFGEICL--LTRGRRTASVRADTYCR 513
Db 609 YHAGESVDLSLCFVSVSGSLEVIQDDEWAILGKGDVFGDFWKEATLAQSCANVRALTYCD 668
QY 514 LYSLSVDHFNVALEPFPMMRRAPF-----TVAMDRLRLRIGKKNSI-----LQKRSEP 561
Db 669 LHVIKRDLALQKLEFYTAFSHSFSRNLILTNLKRIVFRKISDVKREEREMKRNAP 728
QY 562 ---SPGSSGGIMEQHLVQHDRDMARGVRGRAPSTGAQLSGKPKVLWEPLVHAPLQAAVTS 618
Db 729 LILPPDHVRELFRFRQCKEARLAERGGRDLDLDVEKGNVLTE---HASANHSLVKA 785
QY 619 NVAITALTHQRGPLPLSPDSPATILARSNWSRAGSPASPLVPVRAGPASTSLRPPART 678
Db 786 SVVTV-----RESPATVPSFQA-----ASTSGVPD----- 810
QY 679 LHASLSRAGRSQVSLGPPGGGG---RRLGPRGRPL-----SASQPSLPOR- 722
Db 811 -HAKLOAPGS---ECLGPKGGGGCAKRSKWARFKDACGCKSDWNKSKASMETLPT 866
QY 723 -ATDGSFGRKSGSERLPPSGLL-----AKPRTAQPPRP-----PYPE 761
Db 867 KASGEATLKKTDCSDSGITKSDRLDNVGEARSQDRSPILAEVCHSVPIPE 919

RESULT 3
US-11-312-958-18
Sequence 18, Application US/11312958

GenCore version 5.1.9
 Copyright (c) 1993 - 2006 Bioceleration Ltd.
 OM protein - protein search, using sw model
 Run on: June 26, 2006, 20:39:42 ; Search time 23 Seconds
 (without alignments)
 768.802 Million cell updates/sec
 Title: US-09-767-597-1
 Perfect score: 4038
 Sequence: 1 MEAEQRPAGASEGATPGL.....PRPVPEPATRGLQLSANM 774
 Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5
 Searched: 99297 seqs, 22845552 residues
 Total number of hits satisfying chosen parameters: 99297

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Published Applications AA New.*

- 1: /EMC_Celerra_SID3S/prodata/2/pubpaa/US09_NEW_PUB.pep.*
- 2: /EMC_Celerra_SID3S/prodata/2/pubpaa/US06_NEW_PUB.pep.*
- 3: /EMC_Celerra_SID3S/prodata/2/pubpaa/US08_NEW_PUB.pep.*
- 4: /EMC_Celerra_SID3S/prodata/2/pubpaa/US08_NEW_PUB.pep.*
- 5: /EMC_Celerra_SID3S/prodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 6: /EMC_Celerra_SID3S/prodata/2/pubpaa/US10_NEW_PUB.pep.*
- 7: /EMC_Celerra_SID3S/prodata/2/pubpaa/US11_NEW_PUB.pep.*
- 8: /EMC_Celerra_SID3S/prodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	493.5	12.2	694	7	US-11-302-678-26
2	477	11.8	989	7	US-11-312-958-30
3	475.5	11.8	988	7	US-11-312-958-18
4	331	8.2	694	6	US-10-449-902-52909
5	328.5	8.1	502	6	US-10-449-902-53639
6	304.5	7.5	696	6	US-10-449-902-47249
7	267.5	6.6	772	6	US-10-449-902-53398
8	262	6.5	573	6	US-10-449-902-43839
9	260	6.4	628	6	US-10-449-902-45578
10	260	6.4	713	6	US-10-449-902-55070
11	256.5	6.4	639	6	US-10-449-902-29881
12	207	5.1	449	6	US-10-449-902-30986
13	197	4.9	456	6	US-10-449-902-43189
14	194	4.8	343	6	US-10-953-349-19725
15	194	4.8	350	6	US-10-953-349-19724
16	194	4.8	375	6	US-10-953-349-22935
17	165.5	4.1	439	6	US-10-449-902-36615
18	164.5	4.1	215	6	US-10-953-349-19726
19	164	4.1	312	6	US-10-953-349-22936
20	161	4.0	298	6	US-10-953-349-22937
21	160	4.0	386	6	US-10-449-902-53215
22	140.5	3.5	339	6	US-10-953-349-34798
23	140	3.5	206	6	US-10-953-349-25833
24	138	3.4	1327	7	US-11-221-332-48
25	136	3.4	461	6	US-10-449-902-42292

Sequence 2847, Ap
 Sequence 1, Appli
 Sequence 20, Appl
 Sequence 2957, Ap
 Sequence 10919, A
 Sequence 42619, A
 Sequence 31470, A
 Sequence 45786, A
 Sequence 3037, A
 Sequence 2, Appli
 Sequence 7, Appli
 Sequence 17, Appli
 Sequence 27984, A
 Sequence 27983, A
 Sequence 44460, A
 Sequence 41294, A
 Sequence 31843, A
 Sequence 32616, A
 Sequence 14, Appli
 Sequence 34907, A

ALIGNMENTS

RESULT 1
 US-11-302-678-26
 ; Sequence 26, Application US/11302678
 ; Publication No. US20060088881A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Millennium Pharmaceuticals, Inc.
 ; APPLICANT: Silos-Santiago, Immaculada
 ; APPLICANT: Venkateswarlu, Karicheti
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
 ; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1435, 559, 34021, 44099, 25278,
 ; TITLE OF INVENTION: 641, 260, 55089, 21407, 42032, 46656, 62553, 302, 323, MOLECULES.
 ; TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.
 ; FILE REFERENCE: MPI02-012PIRNM OMNI
 ; CURRENT APPLICATION NUMBER: US/11/302,678
 ; CURRENT FILING DATE: 2005-12-14
 ; PRIOR APPLICATION NUMBER: US/10/345,680
 ; PRIOR FILING DATE: 2003-01-16
 ; PRIOR APPLICATION NUMBER: US 60/349,511
 ; PRIOR FILING DATE: 2002-01-18
 ; PRIOR APPLICATION NUMBER: US 60/360,500
 ; PRIOR FILING DATE: 2002-02-28
 ; PRIOR APPLICATION NUMBER: US 60/365,041
 ; PRIOR FILING DATE: 2002-03-15
 ; PRIOR APPLICATION NUMBER: US 60/374,063
 ; PRIOR FILING DATE: 2002-04-19
 ; PRIOR APPLICATION NUMBER: US 60/403,468
 ; PRIOR FILING DATE: 2002-08-14
 ; PRIOR APPLICATION NUMBER: US 60/414,262
 ; PRIOR FILING DATE: 2002-09-27
 ; PRIOR APPLICATION NUMBER: US 60/419,986
 ; PRIOR FILING DATE: 2002-10-21
 ; PRIOR APPLICATION NUMBER: US 60/423,809
 ; PRIOR FILING DATE: 2002-11-05
 ; PRIOR APPLICATION NUMBER: US 60/429,797
 ; PRIOR FILING DATE: 2002-11-26
 ; NUMBER OF SEQ ID NOS: 66
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 26
 ; LENGTH: 694
 ; TYPE: PRT
 ; ORGANISM: Homo Sapiens
 ; US-11-302-678-26

Query Match 12.2%; Score 493.5; DB 7; Length 694;

Best Local Similarity 26.5%; Pred. No. 7.5e-27;

Matches 133; Conservative 106; Mismatches 223; Indels 39; Gaps 10;

QY 74 EOBVRKAGAWIHPYSDRFRFYNDLMLLLVGNLIVLPVGITF--FKRENSPPMIVFNV 131

November 2005

Published Applications Nucleic Acid and Published Applications Amino Acid database searches now generate two sets of results each. The Published Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published Applications New databases; older published applications make up the Published Applications Main databases.

Searches run against Nucleic Acid Published Applications produce two sets of results, with the extensions **.rnpbm** (Published Applications NA_Main) and **.rnpbn** (Published Applications_NA_New). Searches run against Amino Acid Published Applications produce two sets of results, with the extensions **.rapbm** (Published Applications_AA_Main) and **.rapbn** (Published Applications_AA_New).